

Fr m: Ramirez, Delia
S nt: Thursday, August 03, 2006 4:56 PM
To: STIC-Biotech/ChemLib
Subject: 10/612779

Hi,

I would like to request the following search: SEQ ID NO:2 in the protein databases.

Please provide a printout of this search.

Thank you very much.

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Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA#: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.9
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MM protein - protein search, using SW model

run on: August 7, 2005, 09:20:34 ; Search time 92 Seconds
 (without alignments)

3026.574 Million cell updates/sec

title: US-10-612-779-2

effect score: 3086

sequence: MCIVGATAQRDVAELLEG.....LIKGTDVDQPRNTLAKSVTVB 609

scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Abo6174 Klebsiell
 Abu3411 Protein e
 Abu5041 Protein e
 Abu5069 Protein e
 Ads43812 Bacterial
 Adn17785 Bacterial
 Abm70565 Phototroph
 Adf07237 Bacterial
 Abu41104 Protein e
 Aau35425 Haemophil
 Abu30239 Protein e
 Aae30459 Haemophil
 Aee31344 Haemophil
 Abu49139 Protein e
 Abu39464 Protein e
 Abu39730 Protein e
 Ads24814 Bacterial
 Abu33518 Pseudomon
 Abu35924 Protein e
 Abu70418 Pseudomon
 Abu41714 Protein e
 Abu17019 Protein e

ALIGNMENTS

Job processing. Maximum match 3. Listing first 45 summaries

Database : A_Geneseq_8 : * AAY58822

RESULT 1

ID AAY58822 standard; protein; 609 AA.

XX

XX

AC AAY58822;

XX

XX

DT 08-MAY-2000 (first entry)

XX

DE E. coli glucosamine-6-phosphate synthase.

XX

XX

KW Glucosamine-6-phosphate synthase; GICN6P; glucosamine;

KW metabolic engineering; DNA; amide; NKGND2-28

de total

result	SUMMARIES				Description	
	No.	Score	Query Match	Length	DB ID	
1	3086	100.0	609	3	AAU58822	E. coli 9
2	3086	100.0	609	4	AAU34806	E. coli 9
3	3086	100.0	609	6	ABU08829	Protein e
4	3086	100.0	609	8	ADJ38857	Glucosami
5	3086	100.0	609	8	ADDS45181	Bacterial
6	3086	100.0	609	8	ADU00590	Amino aci
7	3081	99.8	608	9	ADW23840	Novel hum
8	3080	99.8	609	3	AAV58827	E. coli 9
9	3080	99.8	609	3	AAV58826	E. coli 9
10	3080	99.8	609	8	ADJ38865	Mutant 91
11	3080	99.8	609	8	ADJ38867	Mutant 91
12	3079	99.8	609	3	AAV58825	E. coli 9
13	3079	99.8	609	8	ADJ38863	Mutant 91
14	3071	99.5	609	3	AAV58823	E. coli 9
15	3071	99.5	609	8	ADJ38859	Mutant 91
16	3068	99.4	609	3	AAV58824	E. coli 9
17	3068	99.4	609	8	ADJ38861	Mutant 91
18	3068	99.4	609	8	ADU00592	Amino aci
19	3061	99.2	609	8	ADJ38869	Mutant 91
20	3053	98.9	609	4	AAU38472	Salmonell
21	3053	98.9	609	6	ABU048228	Protein e
22	2956	95.6	609	4	ADT28355	Klebsiel
23	2876	93.2	609	4	ADT36165	Klebsiel

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, derived by analysis of the total score distribution.

ט' ציון

RESULT 1
AAY58822
ID AAY58822 standard: protein: 60

AY58822;
08-MAY-2000 (first entry)
E. coli glucosamine-6-phosphate synthase.

WO2000004182-A1.

27-JAN-2000. 15-JUL-1999; 15-JUL-1998; (DCV-) DCV INC DBA BIO-TECH RESOURCES. 99WO-US015976. 98US-00115475. Berry A, Burlingame RP, Millis JR, WPI; 2000-182441/16. N-PSDB; AA258249.

Fermentation of *E. coli* having an altered pathway to produce glucosamine, especially

XX PS Claim 15; Page 111-113; 150pp; English.
XX CC The present sequence is that of wild type
CC synthase (GlcN6P synthase) of *Escherichia*
CC *coli*. It is predicted from the isolated GlcN6P gene
CC -28. Recombinant nucleic acids encoding
CC are used for the expression of the enzyme
CC especially *E. coli*. For use in the products
CC invention also provides methods for the
CC using a genetically engineered microorganism
CC modified to increase its activity
CC synthase modifications comprise amino
CC acid substitutions, additions, deletions, and
CC preferred modifications are those that do not
CC significantly alter the enzyme's specificity and
CC activity.

CC	inversion, derivatization or substitution, especially I4T, I272T, S240P, A39T, R250C, G472S and L469P substitution, of the present sequence	XX	PF 21-MAR-2001; 2001WO-US009180.
CC	Sequence 609 AA;	XX	PR 21-MAR-2000; 2000US-0191078P.
PR	Score 3086; DB 3; Length 609;	PR 23-MAY-2000; 2000US-020648P.	
PR	Best Local Similarity 100.0%; Pred. No. 4.7e-264;	PR 26-MAY-2000; 2000US-0207727P.	
PR	Matches 609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	PR 23-OCT-2000; 2000US-0242578P.	
PR	1 MCGIVGAIQDVAEILLLGRLRLEYRGDSAGLAVIDEAGHMTLRLRGKVQMLAQAE 60	PR 27-NOV-2000; 2000US-0253125P.	
PR	1 MCGIVGAIQDVAEILLLGRLRLEYRGDSAGLAVIDEAGHMTLRLRGKVQMLAQAE 60	PR 22-DEC-2000; 2000US-0257331P.	
PR	61 EPLHGGTGAIAHTRWATHGEPSEYNAHPVSEHIVVWINGITENHEPLREELKARGTYFV 120	PR 16-FEB-2001; 2001US-0269308P.	
PR	61 EPLHGGTGAIAHTRWATHGEPSEYNAHPVSEHIVVWINGITENHEPLREELKARGTYFV 120	XX (ELIT-) ELITRA PHARM INC.	
PR	61 EPLHGGTGAIAHTRWATHGEPSEYNAHPVSEHIVVWINGITENHEPLREELKARGTYFV 120	PA PA	
PR	61 EPLHGGTGAIAHTRWATHGEPSEYNAHPVSEHIVVWINGITENHEPLREELKARGTYFV 120	PI Hasebeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;	
PR	61 EPLHGGTGAIAHTRWATHGEPSEYNAHPVSEHIVVWINGITENHEPLREELKARGTYFV 120	PI Yamamoto RT, Xu HH;	
PR	61 EPLHGGTGAIAHTRWATHGEPSEYNAHPVSEHIVVWINGITENHEPLREELKARGTYFV 120	XX WPI; 2001-611445/70.	
PR	61 EPLHGGTGAIAHTRWATHGEPSEYNAHPVSEHIVVWINGITENHEPLREELKARGTYFV 120	DR N-PSDB; AAS52655.	
PR	121 SETDTEVIAHLVNLKQGGTLREAVLRAIPOLRGAYCTGVIMDSRHPDTLAAARSGSPLV 180	XX New Polynucleotides for the identification and development of	
PR	121 SETDTEVIAHLVNLKQGGTLREAVLRAIPOLRGAYCTGVIMDSRHPDTLAAARSGSPLV 180	PT antibiotics, comprise sequences of antisense nucleic acids.	
PR	181 IGLGMGENTASDQLLLPVTRRPFLEGGDIAEITRSVNFDTKTAEVQRQDIESNLQ 240	XX Example 3; SEQ ID NO 10399; 511pp; English.	
PR	181 IGLGMGENTASDQLLLPVTRRPFLEGGDIAEITRSVNFDTKTAEVQRQDIESNLQ 240	XX	
PR	241 YDAGDKGIRHYMKEIYEQPNALKNTLGRISHQVDSLSELGPNADELSKVEHQLA 300	CC The invention relates to antisense inhibitors of genes essential to	
PR	241 YDAGDKGIRHYMKEIYEQPNALKNTLGRISHQVDSLSELGPNADELSKVEHQLA 300	CC prokaryotic cellular proliferation, their use in identifying the genes,	
PR	241 YDAGDKGIRHYMKEIYEQPNALKNTLGRISHQVDSLSELGPNADELSKVEHQLA 300	CC their use in the discovery of novel antibiotics, the essential genes	
PR	241 YDAGDKGIRHYMKEIYEQPNALKNTLGRISHQVDSLSELGPNADELSKVEHQLA 300	CC themselves and the encoded proteins. The prokaryotes used are Escherichia	
PR	301 CGTYSNSGIVSRYWESLGIPIPDCVTEIASEFRYRKSAYVRNSLMITLQSGETADTLAGL 360	CC coli, <i>Staphylococcus aureus</i> , <i>Salmonella typhi</i> , <i>Klebsiella pneumoniae</i> ,	
PR	301 CGTYSNSGIVSRYWESLGIPIPDCVTEIASEFRYRKSAYVRNSLMITLQSGETADTLAGL 360	CC <i>Pseudomonas aeruginosa</i> and <i>Enterococcus faecalis</i> . The invention is also	
PR	301 CGTYSNSGIVSRYWESLGIPIPDCVTEIASEFRYRKSAYVRNSLMITLQSGETADTLAGL 360	CC useful for the identification of potential new targets for antibiotic	
PR	361 RLSKELGYGLSALCNVPPSLLYRESDLALMTNAGTEIGVASTKAFTTQLTVLMLVAKL 420	CC development. The antisense nucleic acids can also be used to identify	
PR	361 RLSKELGYGLSALCNVPPSLLYRESDLALMTNAGTEIGVASTKAFTTQLTVLMLVAKL 420	CC proteins used in proliferation, to express these proteins, and to obtain	
PR	421 SRLKGLDASIEHDIVHGLQALPSRQEOMLSQDKRIBEAEDSDKHALFLGRGDQYPIA 480	CC antibodies capable of binding to the expressed proteins. The proteins can	
PR	421 SRLKGLDASIEHDIVHGLQALPSRQEOMLSQDKRIBEAEDSDKHALFLGRGDQYPIA 480	CC be used to screen compounds in rational drug discovery programmes. The	
PR	421 SRLKGLDASIEHDIVHGLQALPSRQEOMLSQDKRIBEAEDSDKHALFLGRGDQYPIA 480	CC antisense nucleic acid sequence is also useful to screen for homologous	
PR	481 LEGALKLKEISYTHAEAYAAGELRKHPPLIDADMPVIVAVPNELLEKLSNIEEVRAR 540	CC nucleic acids which are required for cell proliferation in a wide variety	
PR	481 LEGALKLKEISYTHAEAYAAGELRKHPPLIDADMPVIVAVPNELLEKLSNIEEVRAR 540	CC of organisms. The present sequence represents an essential prokaryotic	
PR	601 NLAKSVTVE 609	CC cellular proliferation protein. Note: The sequence data for this patent	
PR	601 NLAKSVTVE 609	CC did not form part of the printed specification, but was obtained in	
PR	601 NLAKSVTVE 609	CC electronic format directly from WIPO at	
PR	601 NLAKSVTVE 609	CC ftp.wipo.int/pub/published_pct_sequences	
PR	601 NLAKSVTVE 609	XX Sequence 609 AA;	
PR	601 NLAKSVTVE 609	Query Match 100.0%; Score 3086; DB 4; Length 609;	
PR	601 NLAKSVTVE 609	Best Local Similarity 100.0%; Pred. No. 4.7e-264;	
PR	601 NLAKSVTVE 609	Matches 609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
PR	61 EPLHGGTGAIAHTRWATHGEPSEYNAHPVSEHIVVWINGITENHEPLREELKARGTYFV 120	QY 1 MCGIVGAIQDVAEILLLGRLRLEYRGDSAGLAVIDEAGHMTLRLRGKVQMLAQAE 60	
PR	61 EPLHGGTGAIAHTRWATHGEPSEYNAHPVSEHIVVWINGITENHEPLREELKARGTYFV 120	DB 1 MCGIVGAIQDVAEILLLGRLRLEYRGDSAGLAVIDEAGHMTLRLRGKVQMLAQAE 60	
PR	121 SETDTEVIAHLVNLKQGGTLREAVLRAIPOLRGAYCTGVIMDSRHPDTLAAARSGSPLV 180	QY 121 SETDTEVIAHLVNLKQGGTLREAVLRAIPOLRGAYCTGVIMDSRHPDTLAAARSGSPLV 180	
PR	121 SETDTEVIAHLVNLKQGGTLREAVLRAIPOLRGAYCTGVIMDSRHPDTLAAARSGSPLV 180	DB 121 SETDTEVIAHLVNLKQGGTLREAVLRAIPOLRGAYCTGVIMDSRHPDTLAAARSGSPLV 180	
PR	181 IGLGMGENTASDQLLLPVTRRPFLEGGDIAEITRSVNFDTKTAEVQRQDIESNLQ 240	QY 181 IGLGMGENTASDQLLLPVTRRPFLEGGDIAEITRSVNFDTKTAEVQRQDIESNLQ 240	
PR	181 IGLGMGENTASDQLLLPVTRRPFLEGGDIAEITRSVNFDTKTAEVQRQDIESNLQ 240	DB 181 IGLGMGENTASDQLLLPVTRRPFLEGGDIAEITRSVNFDTKTAEVQRQDIESNLQ 240	
PR	241 YDAGDKGIRHYMKEIYEQPNALKNTLGRISHQVDSLSELGPNADELSKVEHQLA 300	QY 241 YDAGDKGIRHYMKEIYEQPNALKNTLGRISHQVDSLSELGPNADELSKVEHQLA 300	
PR	241 YDAGDKGIRHYMKEIYEQPNALKNTLGRISHQVDSLSELGPNADELSKVEHQLA 300	DB 241 YDAGDKGIRHYMKEIYEQPNALKNTLGRISHQVDSLSELGPNADELSKVEHQLA 300	
PR	301 CGTYSNSGIVSRYWESLGIPIPDCVTEIASEFRYRKSAYVRNSLMITLQSGETADTLAGL 360	QY 301 CGTYSNSGIVSRYWESLGIPIPDCVTEIASEFRYRKSAYVRNSLMITLQSGETADTLAGL 360	
PR	301 CGTYSNSGIVSRYWESLGIPIPDCVTEIASEFRYRKSAYVRNSLMITLQSGETADTLAGL 360	DB 301 CGTYSNSGIVSRYWESLGIPIPDCVTEIASEFRYRKSAYVRNSLMITLQSGETADTLAGL 360	
PR	361 RLSKELGYGLSALCNVPPSLLYRESDLALMTNAGTEIGVASTKAFTTQLTVLMLVAKL 420	QY 361 RLSKELGYGLSALCNVPPSLLYRESDLALMTNAGTEIGVASTKAFTTQLTVLMLVAKL 420	

Db 361 RLSKELGYGSLATCNVPPSSLVRESDLALMTNAGTEIGVASTRAFTTOLVILMVALR 420
 Qy 421 SRLKLDASIEHDVHGLQALPSRTEQMSQDRKIEALLEDFSDKHHALFLGRGDQYTA 480
 Db 422 SRLKLDASIEHDVHGLQALPSRTEQMSQDRKIEALAEFDSDKHHALFLGRGDQYTA 480
 Qy 481 LEGALKLKEISYIHAAYAAGELKGPLALIDAMPVIVAPNELLKSNIEEVRA 540
 Db 481 LEGALKLKEISYIHAAYAAGELKGPLALIDAMPVIVAPNELLKSNIEEVRA 540
 Qy 541 GGQLXVFAQDAGFVSSDNMHIEMPHVEIPIFYTPLQLLAYHVALIKGTDVQPR 600
 Db 541 GGQLXVFAQDAGFVSSDNMHIEMPHVEIPIFYTPLQLLAYHVALIKGTDVQPR 600
 Qy 601 NLAKSVTVE 609
 Db 601 NLAKSVTVE 609

RESULT 3

ABU26829 ABU26829 standard; protein; 609 AA.

AC ABU26829;

XX DT 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #14356.

XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX OS Escherichia coli.

XX WO200277183-A2.

XX PD 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00615242.

PR 06-SEP-2001; 2001US-00548993.

PR 25-OCT-2001; 2001US-03429239.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX PA Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI: 2003-029926/02.

XX DR -PSDB; ACA2699.

PT New antisense nucleic acids useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 56753; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8)

identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp://wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences)

Sequence 609 AA:

Query	Match	Score	DB	Length
Qy	1 MCGIVGATAQDVAEILLEGRLLERYGVDAGLVIDAGEMTRLRLGKQVMLAQAE	100.0%	6	609;
Db	1 MCGIVGATAQDVAEILLEGRLLERYGVDAGLVIDAGEMTRLRLGKQVMLAQAE	100.0%	6	609;
Qy	61 EHPLHGGTGAIAHTRWATHGEPESEVNAPHVSEHIVVHNGTIEHENPDRREELKARGTTFV	61	120	
Db	61 EHPLHGGTGAIAHTRWATHGEPESEVNAPHVSEHIVVHNGTIEHENPDRREELKARGTTFV	61	120	
Qy	121 SETDTEVIAHLYNWLKGGLTRBAVLRAPOLRGAGTVMDSRHPTTLLAARSGLSPV	121	180	
Db	121 SETDTEVIAHLYNWLKGGLTRBAVLRAPOLRGAGTVMDSRHPTTLLAARSGLSPV	121	180	
Qy	181 IGLGMGENFIASQQLALLPVTRRFLEGDAEITTRSVDNFDKTGAEVKRDIESNLQ	181	240	
Db	181 IGLGMGENFIASQQLALLPVTRRFLEGDAEITTRSVDNFDKTGAEVKRDIESNLQ	181	240	
Qy	241 YDAGDKGIGYRHYMOKETYEQPNAIKNTLGRISHGQYDLSSELGPNADELLSKYEHQIILA	241	300	
Db	241 YDAGDKGIGYRHYMOKETYEQPNAIKNTLGRISHGQYDLSSELGPNADELLSKYEHQIILA	241	300	
Qy	301 CGTSYNSGMVSRVWESLAGIPCDVETAEFRYRKSAVTRNSLMTLSQSGETADTLAGL	301	360	
Db	301 CGTSYNSGMVSRVWESLAGIPCDVETAEFRYRKSAVTRNSLMTLSQSGETADTLAGL	301	360	
Qy	361 RLSKELGYGSLATCNVPESSLVRESDALMTNAGTEIGVASTKAPTTQLTVILMVALR	361	420	
Db	361 RLSKELGYGSLATCNVPESSLVRESDALMTNAGTEIGVASTKAPTTQLTVILMVALR	361	420	
Qy	421 SRLKGLDASIEHDVHGLQALPSRTEQMSQDRKIEALLEDFSDKHHALFLGRGDQYTA	421	480	
Db	421 SRLKGLDASIEHDVHGLQALPSRTEQMSQDRKIEALLEDFSDKHHALFLGRGDQYTA	421	480	
Qy	481 LEGALKLKEISYIHAAYAAGELKGPLALIDAMPVIVVAPNELLKSNIEEVRA	481	540	
Db	481 LEGALKLKEISYIHAAYAAGELKGPLALIDAMPVIVVAPNELLKSNIEEVRA	481	540	
Qy	541 GGOLYVFAQDAGFVSSDNMHTIEMPHVEVTAPIFYTPLQLLAYVALIKGTDVQPR	541	600	
Db	541 GGOLYVFAQDAGFVSSDNMHTIEMPHVEVTAPIFYTPLQLLAYVALIKGTDVQPR	541	600	
Qy	601 NLAKSVTVE	601	609	
Db	601 NLAKSVTVE	601	609	

RESULT 4
 AD138857 AD138857 standard; protein; 609 AA.

ID AD138857

CC The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 609 AA;

Query Match 100.0%; Score 3086; DB: 8; Length 609;
Best Local Similarity 100.0%; Pred. No. 4.7e-264;
Matches 609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCGIVGAIQDVARILLELRLRRLRRLRRLRRLRRLRRLRQLVQMLAQAE 60
Db 1 MCGIVGAIQDVARILLELRLRRLRRLRRLRRLRQLVQMLAQAE 60
Qy 61 EPLHGGTGTGAHTRWATHGEPEVSENAHPVSEHIVVWVINGIIEHENPRLRLKARGYTFV 120
Db 61 EPLHGGTGTGAHTRWATHGEPEVSENAHPVSEHIVVWVINGIIEHENPRLRLKARGYTFV 120
Qy 121 SETDTEVIAHLVNLWKLQGGTTLREAVRLAIPQLRGAYGTIVIMDSRHPDTLIAARSGSPIV 180
Db 121 SETDTEVIAHLVNLWKLQGGTTLREAVRLAIPQLRGAYGTIVIMDSRHPDTLIAARSGSPIV 180
Db 181 IGLGMGENFTASDQLLPTTRFLFEDGIAITRSPNINIFKTKGAVKRDIESNQ 240
Db 181 IGLGMGENFTASDQLLPTTRFLFEDGIAITRSPNINIFKTKGAVKRDIESNQ 240
Qy 241 YDAGDKGIRYHMOKEIYIOPNAIKNTLGRISHQVDLSELGNADELISKVHIIQIA 300
Db 241 YDAGDKGIRYHMOKEIYIOPNAIKNTLGRISHQVDLSELGNADELISKVHIIQIA 300
Qy 301 CGTSTNSGKMSRYMPESLGIACPCDVEIASEFRYKSAVRNSLMTLSOSGETADTLQL 360
Db 301 CGTSTNSGKMSRYMPESLGIACPCDVEIASEFRYKSAVRNSLMTLSOSGETADTLQL 360
Qy 361 RLSKRLGCGSLAIACNVPSSVLVRESDLALMTNGTEIGVASTKAFTQTLVLMVAKL 420
Db 361 RLSKRLGCGSLAIACNVPSSVLVRESDLALMTNGTEIGVASTKAFTQTLVLMVAKL 420
Qy 421 SRLKGLDASIEHDIVHGLQALPSRTEQMLSQDKRIEALDFDSKGHALFLGRGDDQYPPA 480
Db 421 SRLKGLDASIEHDIVHGLQALPSRTEQMLSQDKRIEALDFDSKGHALFLGRGDDQYPPA 480
Qy 481 LEGALKLKKEIYSIYHAAVAGELKHPGLLIDADMPTVIAVAPNELLKLKSNIEEVVAR 540
Db 481 LEGALKLKKEIYSIYHAAVAGELKHPGLLIDADMPTVIAVAPNELLKLKSNIEEVVAR 540
Qy 541 GGQLYVFAADDAGFSSDNNHIIEMPVTEVIAPIFYTPQLAYHAIKGDVQPR 600
Db 541 GGQLYVFAADDAGFSSDNNHIIEMPVTEVIAPIFYTPQLAYHAIKGDVQPR 600
Qy 601 NLAKSVTVE 609

Db 601 NLAKSVTVE 609
RESULT 6
ADDU0590 standard; protein; 609 AA.
ID ADDU0590
XX
AC ADDU0590;
XX DT 13-JAN-2005 (first entry)
XX Amino acid sequence of a glucosamine-6-phosphate synthase.
XX chitin; chitosan; fermentation;
XX Glutamine-fructose-6-phosphate amidotransferase; glucosamine synthetase;
XX chitosamine-6-phosphate synthase; GFA1 gene; gfmS gene;
XX Glucosamine-6-phosphate acetyltransferase; GNA1 gene; chitin synthase;
XX chitin deacetylase; CDA1 gene; CDA2 gene;
XX N-acetylglucosamine-6-phosphate deacetylase;
XX Glucosamine-6-phosphate deaminase; chitinase; chitosanase; fungus; yeast;
XX enzyme.
XX Escherichia coli.
XX OS
XX PN WO2004092391-A2.
XX PD 28-OCT-2004.
XX PPT 12-APR-2004; 2004WO-US011286.
XX PR 11-APR-2003; 2003US-0462087P.
PA (ARRI-1) ARKION LIFE SCI LLC.
XX PI Derg M, McMullin TW, Grund AD;
XX DR WPI: 2004-766880/75.
DR N-PSDB; ADDU0590.
XX PS Example 1; SEQ ID NO 23; 161PP; English.
XX The specification describes method for producing chitin or chitosan by a fermentation process. The method involves culturing in a fermentation medium a microorganism which comprises one or more genetic modifications that result in an increase in the activity of N-acetylglucosamine-6-phosphate amidotransferase (also known as glucosamine synthetase and glucosamine-6-phosphate synthase, and encoded by the GFA1 eukaryotic gene and the gfmS bacterial gene), glucosamine-6-phosphate acetyltransferase (encoded by GNA1), chitin synthase or chitin deacetylase (encoded by CDA1 and CDA2), or in decrease in the activity of N-acetylglucosamine-6-phosphate deacetylase, glucosamine-6-phosphate diamine, chitinase and chitosanase, and collecting the chitin or chitosan. The method is useful for producing chitin or chitosan by utilizing microorganisms such as fungi, yeast (e.g. *Saccharomyces* or *Schizosaccharomyces*), and filamentous fungus (e.g. *Aspergillus*, *Absidia* or *Rhizopus*), preferably *S. cerevisiae*, *A. niger* or *A. nidulans*. The method enables high quantities of chitin and chitosan to be produced cost effectively. The present sequence represents an *Escherichia coli* glucosamine-6-phosphate synthase. It was used to transform yeast for use in the method of the invention.
XX SQ Sequence 609 AA;
Query Match 100.0%; Score 3086; DB: 8; Length 609;
Best Local Similarity 100.0%; Prod. No. 4.7e-264;
Matches 609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCGIVGATAQDVAEILLELRLRRLRRLRQLVQMLAQAE 60

Db	1	MCGIVGAIJAQDVAEITLLEGLRRLRLEYRGYDSSAGLAVVDAEGHMTRRLRGKVOMLAQAAE	60	XX	PT	New modified glutamine:fructose-6-phosphate amidotransferase, useful for
Qy	61	EPBLHGCTGIAKTRWATHGESEVNAHYPSEHIVVANGLIEHREPLEELKARGTYFV	120	PT	identifying specific inhibitors. Potentially useful for treating e.g.	
Db	61	EPBLHGCTGIAKTRWATHGESEVNAHYPSEHIVVANGLIEHREPLEELKARGTYFV	120	PT	diabetes, contains a purification tag, also related nucleic acid	
XX				XX		
PS				PS		Disclosure; SEQ ID NO 13; 61pp; French.
XX				XX		
Db	121	SETDTDEVIAHLYNWEKLGGTIREAVYLTFPQLRGAYGTVIMDSRHPDTLAAARSQSPV	180	CC	This invention relates to a novel protein corresponding to human	
Db	121	SETDTDEVIAHLYNWEKLGGTIREAVYLTFPQLRGAYGTVIMDSRHPDTLAAARSQSPV	180	CC	enzymatically active but modified glutamine:fructose-6-phosphate	
Qy	181	IGLMGENFIASDQLALLPTVTRRFLEEDIAETTRSYNIFDTKGAVFKRQDIESNLQ	240	CC	amidotransferase (GFAT). The invention may be useful for the production	
Db	181	IGLMGENFIASDQLALLPTVTRRFLEEDIAETTRSYNIFDTKGAVFKRQDIESNLQ	240	CC	of compounds with an anti-diabetic, anorectic, metabolic, cycostatic,	
Qy	241	YDAGDKGIVRYHMQKEIYEQPNALIQTNTGPBISHQDVSSELGNADELLSKVHEIQLA	300	CC	osteopathic, fungicide or herbicide activity. The invention may be used	
Db	241	YDAGDKGIVRYHMQKEIYEQPNALIQTNTGPBISHQDVSSELGNADELLSKVHEIQLA	300	CC	to screen for agents that modify, especially inhibit, its activity,	
Qy	301	CGTTSYNSGMSYRWSFESLAGIPCDVIAESFRYKSAVFRNSLMTLSQSGETADTLAGL	360	CC	potentially useful as agents for treatment or prevention of diabetes	
Db	301	CGTTSYNSGMSYRWSFESLAGIPCDVIAESFRYKSAVFRNSLMTLSQSGETADTLAGL	360	CC	(particularly type II), obesity, acidosis, ketosis, cancer and	
Qy	361	RLSKEIYGLSLSLAINVPGSSLVRESDLALMTNAGTEICVASTAKFTQLTVLMLYAKL	420	CC	osteoporosis. In addition, inhibitors of plant and fungal GFAT may be	
Db	361	RLSKEIYGLSLSLAINVPGSSLVRESDLALMTNAGTEICVASTAKFTQLTVLMLYAKL	420	CC	useful as herbicides and fungicides, respectively. The present sequence	
Qy	421	SRLKGLDASIEHDIVHGLQALPSR1TEQMLISODKRIEALADEFSDKHHAFLGRCQDQPLA	480	XX	is that of a human GFAT-like protein of the invention.	
Db	421	SRLKGLDASIEHDIVHGLQALPSR1TEQMLISODKRIEALADEFSDKHHAFLGRCQDQPLA	480	XX	Sequence 608 AA;	
Qy	481	LEGALKLKEISYIHAAYAAGELKGPLAIDADMPVIVAPNELLKELKSNIEEVYR	540	Qy	2 CGIVGAIJAQDVAEITLLEGLRRLRLEYRGYDSSAGLAVVDAEGHMTRRLRGKVOMLAQAAE	61
Db	481	LEGALKLKEISYIHAAYAAGELKGPLAIDADMPVIVAPNELLKELKSNIEEVYR	540	Db	1 CGIVGAIJAQDVAEITLLEGLRRLRLEYRGYDSSAGLAVVDAEGHMTRRLRGKVOMLAQAAE	60
Qy	541	GGOLYVFAQQDAGFVSSDNMHIEMPHYEEVIAPIFYVPLQLAYVALIKGTDVDQPR	600	Qy	62 HPLHGCTGIAKTRWATHGESEVNAHYPSEHIVVANGLIEHREPLEELKARGTYFV	121
Db	541	GGOLYVFAQQDAGFVSSDNMHIEMPHYEEVIAPIFYVPLQLAYVALIKGTDVDQPR	600	Db	61 HPLHGCTGIAKTRWATHGESEVNAHYPSEHIVVANGLIEHREPLEELKARGTYFV	120
Qy	601	NLAKSVTVE	609	Qy	122 ETDTDEVIAHIVVNLKQGQTTLREAVLRLPQGTTLREAVLRLPQGAYTIVMDSRHPDTLAAARSQPLV	181
Db	601	NLAKSVTVE	609	Db	121 ETDTDEVIAHIVVNLKQGQTTLREAVLRLPQGAYTIVMDSRHPDTLAAARSQPLV	180
Qy	7	RESULT 7		Qy	182 GLGMGBNFIASDOLALLPTVTRRFLEEGDIAETRSYNIFDKTKGAEVKRODIESNLQY	241
ADW23840		ADW23840 standard; protein; 608 AA.		Db	181 GLGMGBNFIASDOLALLPTVTRRFLEEGDIAETRSYNIFDKTKGAEVKRODIESNLQY	240
XX				Qy	242 DAGDKGIVRYHMQKEIYEQPNALIQTNTLGRISHQDQVPLSELGPNADELLSKVHEIQLAC	301
AC				Db	241 DAGDKGIVRYHMQKEIYEQPNALIQTNTLGRISHQDQVPLSELGPNADELLSKVHEIQLAC	300
XX				Qy	302 GTSYNSGMSYRWSFESLAGIPCDVIAESFRYKSAVFRNSLMTLSQSGETADTLAGL	361
XX				Db	301 GTSYNSGMSYRWSFESLAGIPCDVIAESFRYKSAVFRNSLMTLSQSGETADTLAGL	360
DT	07-APR-2005	(first entry)		Qy	362 LSKEIYGLSLSAICNPGSSLVRESDLALMTNAGTEICVASTAKFTQLTVLMLYAKL	421
XX				Db	361 LSKEIYGLSLSAICNPGSSLVRESDLALMTNAGTEICVASTAKFTQLTVLMLYAKL	420
DE	Novel human GFAT protein-related E. coli GFAT protein SeqID13.			Qy	422 RLKGLDASIEHDIVHGLQALPSR1TEQMLISODKRIEALADEFSDKHHAFLGRCQDQYPTAL	481
XX	protein purification; glutamine:fructose-6-phosphate amidotransferase;			Db	421 RLKGLDASIEHDIVHGLQALPSR1TEQMLISODKRIEALADEFSDKHHAFLGRCQDQYPTAL	480
KW	antidiabetic; anorectic; metabolic; cycostatic; osteopathic;			Qy	482 EGALKLKEISYIHAAYAAGELKGPLAIDADMPVIVAPNELLKELKSNIEEVYARG	541
KW	fungicide; herbicide; diabetes; non-insulin dependent diabetes;			Db	481 EGALKLKEISYIHAAYAAGELKGPLAIDADMPVIVAPNELLKELKSNIEEVYARG	540
KW	acidosis; cancer; osteoporosis.			Qy	542 GQLYVFAODAGFVSSDNMHIEMPHYEEVIAPIFYVPLQLAYVALIKGTDVDQPRN	601
XX	Escherichia coli.			Db	541 GQLYVFAODAGFVSSDNMHIEMPHYEEVIAPIFYVPLQLAYVALIKGTDVDQPRN	600
XX	PR285734-A1.			Qy	602 LAKSVTVE	609
XX	08-JUL-2003; 2003FR-00008350.			Db	601 LAKSVTVE	608
XX	08-JUL-2003; 2003FR-00008350.			Qy		
(CNRS)	CNRS CENT NAT RECH SCI.			Qy		
PA	Badet DMAJE, Badet BF;			Qy		
PA	WPI; 2005-076419/09.			Qy		
PA	RESULT 8			Qy		
PA	AA58827			Qy		
PA	ID AAY58827 standard; protein; 609 AA.			Qy		

AC	AAY58827;	Qy	301 CGTSSYNGMVSRYWFFBSLAGIFCDVETASEFPRKSAVRNSLIMTISOSGETADTLGL	360
CC		Db	301 CGTSSYNGMVSRYWFFBSLAGIFCDVETASEFPRKSAVRNSLIMTISOSGETADTLGL	360
DT	08-MAY-2000 (first entry)	Qy	361 RLSKEIIGYLGSIAICHNPSSILVRESDPLAMTNAGCTTCAVASTKAFTTQLTIVLMLVAKL	420
TT	E. coli glucosamine-6-phosphate synthase mutant GlcN6P-S-151.	Db	361 RLSKEIIGYLGSIAICHNPSSILVRESDPLAMTNAGCTTCAVASTKAFTTQLTIVLMLVAKL	420
CC	Glucosamine-6-phosphate synthase; <i>glms</i> gene; mutant; GlcN6P-S-151; glucosamine; metabolic engineering; plasmid pKLN23-151; mutant. Escherichia coli.	Qy	421 SRLKGDDASIEHDIVGLOALPSRIEOMLSQDKR1EALAESDSDKHALPLSRGDQYPIA	480
CC	Key Location/Qualifiers	Db	421 SRLKGDDASIEHDIVGLOALPSRIEOMLSQDKR1EALAESDSDKHALPLSRGDQYPIA	480
CC	Misc-difference 472 /note= "replaces wild-type Gly"	Qy	481 LEGALIKE1EISYTHAAYAAEGLKHGPFLALIDAMPVIVVAPNNELLEKLSNIEVYR	540
CC	WO200004182-A1.	Db	481 LEGALIKE1EISYTHAAYAAEGLKHGPFLALIDAMPVIVVAPNNELLEKLSNIEVYR	540
CC	27-JAN-2000.	Qy	541 GGQLYYADQDAGFVSSDNMHLIEMPHVEEVIAPIFYVPLQLLAVHVALIKGTDDQPR	600
CC	15-JUL-1999;	Db	541 GGQLYYADQDAGFVSSDNMHLIEMPHVEEVIAPIFYVPLQLLAVHVALIKGTDDQPR	600
CC	15-JUL-1999;	Qy	601 NLAKSTVTE	609
CC	15-JUL-1999;	Db	601 NLAKSTVTE	609
CC	(DCVB-) DCV INC DBA BIO-TECH RESOURCES.	RESULT 9		
CC	Berry A, Burlingame RP, Millis JR;	ID	AAY58826 standard; protein; 609 AA.	
CC	WPI; 2000-182441/16.	XX	AAY58826	
CC	N-PSDB; AR58254.	AC	AAY58826;	
CC	Fermentation of <i>E. coli</i> having an altered amino acid sugar metabolic pathway to produce glucosamine, especially using novel recombinant glucosamine-6-phosphate synthases.	XX	XX	(first entry)
CC	Claim 28; Page 143-145; 150pp; English.	DT	08-MAY-2000	
CC	The present sequence is that of a mutant, denoted GlcN6P-S-151, of the glucosamine-6-phosphate synthase (GlcN6P synthase) of <i>Escherichia coli</i> . When compared with the wild-type sequence (see AAY58822), the mutant includes a Ser for Gly-472 amino acid substitution. This alteration was predicted from the mutated <i>glms</i> gene in plasmid pKLN23-151 (see AAY58824). The invention provides methods for the overproduction of glucosamine by fermentation using a genetically engineered microorganism, especially <i>E. coli</i> , that includes a modified GlcN6P synthase. Production of the glucosamine by recombinant strain 2123-149 (pKLN23-149) was marginally increased when compared to a strain expressing wild-type GlcN6P synthase sequence 609 AA;	XX	XX	
CC	Sequence 609 AA;	XX	XX	
CC	Query Match 99.8%; Score 3080; DB 3; Length 609;	XX	XX	
CC	Best Local Similarity 99.8%; Pred. No. 1.6e-263;	XX	XX	
CC	Matches 608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	XX	XX	
CC	1 MCGIVGAIQARDVAEILLEGRLRRLYRGDSAGLAVVDAEGHMTTRRLGRVQMLAQAAE	PA	(DCVB-) DCV INC DBA BIO-TECH RESOURCES.	
CC	1 MCGIVGAIQARDVAEILLEGRLRRLYRGDSAGLAVVDAEGHMTTRRLGRVQMLAQAAE	PI	Berry A, Burlingame RP, Millis JR;	
CC	61 EHPLH6G7GIAHTRWATHGEPEVNNAHPHSEHIVVNGTENHEPLRFLKARGTYFV	XX	WPI; 2000-182441/16.	
CC	61 EHPLH6G7GIAHTRWATHGEPEVNNAHPHSEHIVVNGTENHEPLRFLKARGTYFV	DR	N-PSDB; AAZ58233.	
CC	120	XX		
CC	61 EHPLH6G7GIAHTRWATHGEPEVNNAHPHSEHIVVNGTENHEPLRFLKARGTYFV	PT		
CC	120	PT	Fermentation of <i>E. coli</i> having an altered amino acid sugar metabolic pathway to produce glucosamine, especially using novel recombinant variant glucosamine-6-phosphate synthases.	
CC	121 SETDTEVIAHLVNLWKLKGQTIREAVLRAIPLQRGAYTVIMDSRHPDTLAAARSQSPIV	XX	Claim 28; Page 137-139; 150pp; English.	
CC	121 SETDTEVIAHLVNLWKLKGQTIREAVLRAIPLQRGAYTVIMDSRHPDTLAAARSQSPIV	PS		
CC	181 IGLGMGENFIAISDQLAIIPLPRTTRFLIEGDTIAETTRRSNIFDKTGAEYQRDIESNLQ	XX		
CC	181 IGLGMGENFIAISDQLAIIPLPRTTRFLIEGDTIAETTRRSNIFDKTGAEYQRDIESNLQ	CC	The present sequence is that of a mutant, denoted GlcN6P-S-149, of the glucosamine-6-phosphate synthase (GlcN6P synthase) of <i>Escherichia coli</i> .	
CC	181 IGLGMGENFIAISDQLAIIPLPRTTRFLIEGDTIAETTRRSNIFDKTGAEYQRDIESNLQ	CC	When compared with the wild-type sequence (see AAY58822), the mutant includes a Ser for Gly-472 amino acid substitution. This alteration was predicted from the mutated <i>glms</i> gene in plasmid pKLN23-149 (see AAY58823).	
CC	241 YDAGDKGIVRYMOKEYQDPAIAKNTLGRISHGQYDLSLGPNADELSKVETIQLA	CC	The invention provides methods for the overproduction of glucosamine by fermentation using a genetically engineered microorganism, especially <i>E. coli</i> .	
CC	241 YDAGDKGIVRYMOKEYQDPAIAKNTLGRISHGQYDLSLGPNADELSKVETIQLA	CC	CC	

CC coli, that includes a modified GlcN6P synthase. Production of the
 CC glucosamine by recombinant strain 2123-149 (PKUN23-149) was marginally
 XX increased when compared to a strain expressing wild-type GlcN6P synthase

Sequence 609 AA;

Query Match 99.8%; Score 3080; DB 3; Length 609;
 Best Local Similarity 99.8%; Pred. No. 1; Ge-263;
 Matches 608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MCGIVGATIQRDVAEILLEGRLRRLERYGDSAGLAVIDAEGMTTRLRLGKQMLAAAE 60
 Db 1 MCGIVGATIQRDVAEILLEGRLRRLERYGDSAGLAVIDAEGMTTRLRLGKQMLAAAE 60
 Qy 61 EHPLHGCTGIAHTWATHGEPSEVNAHPVSEIIVVNGIENHEPLREELKARGTYFV 120
 Db 61 EHPLHGCTGIAHTWATHGEPSEVNAHPVSEIIVVNGIENHEPLREELKARGTYFV 120
 Qy 121 SETDTEVIAHLVNLWELKQGTLREAVELAIPQRGAVTVIDMSRHDPTLLAARSQSPV 180
 Db 121 SETDTEVIAHLVNLWELKQGTLREAVELAIPQRGAVTVIDMSRHDPTLLAARSQSPV 180
 Qy 182 IGLGMGENTIASDOLALLFVTRFLFEEGDDIAETTRSVNIFDKTGAEVQRQDIESNLQ 240
 Db 181 IGLGMGENTIASDOLALLFVTRFLFEEGDDIAETTRSVNIFDKTGAEVQRQDIESNLQ 240
 Qy 241 YDAGDKGTYRHYNQKEYQPNIAKNTLTKRISHQVDLSELGPNADELSKVEHTQIQA 300
 Db 241 YDAGDKGTYRHYNQKEYQPNIAKNTLTKRISHQVDLSELGPNADELSKVEHTQIQA 300
 Qy 301 CGTSYNSGMVSYRWFESLAGIIPDVEIAESFRYRKSAVRNSLMTISQSGETADPLAGL 360
 Db 301 CGTSYNSGMVSYRWFESLAGIIPDVEIAESFRYRKSAVRNSLMTISQSGETADPLAGL 360
 Qy 361 RLSELGLTGSLSLAICNVPSSSLYRESDLALMTNAGTEIGVASTKRAFTQTLVLLMVLAKL 420
 Db 361 RLSELGLTGSLSLAICNVPSSSLYRESDLALMTNAGTEIGVASTKRAFTQTLVLLMVLAKL 420
 Qy 422 SRLKGLDASIEHDIVHGLQALPSRIEQMISODKRIEALADEFSDKHHALFLGRGDQYPIA 480
 Db 421 SRLKGLDASIEHDIVHGLQALPSRIEQMISODKRIEALADEFSDKHHALFLGRGDQYPIA 480
 Qy 481 LEGALKLKEISYTHAAYAAGELKHGPPLAIDAMPVYVARNELLEKLSNIEVRAR 540
 Db 481 LEGALKLKEISYTHAAYAAGELKHGPPLAIDAMPVYVARNELLEKLSNIEVRAR 540
 Qy 541 GGOLYVFAODQAGEVSSDMHIIEMPHVEVIAPIFYVPLQLLAYVALIKGTVDQPR 600
 Db 541 GGQIYVFAODQAGEVSSDMHIIEMPHVEVIAPIFYVPLQLLAYVALIKGTVDQPR 600
 Qy 601 NLAKSVTVE 609
 Db 601 NLAKSVTVE 609

RESULT 10

ID AD138865 standard protein; 609 AA.
 XX AD138865;
 XX DT 15-APR-2004 (First entry)
 XX DE Mutant glucosamine-6-phosphate synthase, SEQ ID 10.
 XX Glucosamine; N-acetylglucosamine; fermentation;
 KW Glucosamine-6-phosphate acetyltransferase;
 KW Glucosamine-1-phosphate N-acetyltransferase; glucosamine-6-phosphate;
 KW Glucosamine-1-phosphate; N-acetylglucosamine-1-phosphate;
 KW N-acetylglucosamine-6-phosphate; enzyme;
 XX Escherichia coli.

OS

Sequence 609 AA;

OS XX Synthetic.
 PN XX WO2004003175-A2.
 XX PD 08-JAN-2004.
 XX PF 01-JUL-2003; 2003WO-US020925.
 XX PR 01-JUL-2002; 2002US-039348P.
 PA (ARKI-) ARKION LIFE SCI LLC.
 XX PI Deng M, Angerer JD, Cyron D, Grund AD, Jerrall TA, Leanna C,
 Mathe O, Rossen R, Running J, Severson D, Song L, Wassink S;
 XX WPI; 2004-203380/19.
 DR N-PSDB; ADI138864.
 XX PT Producing glucosamine or N-acetylglucosamine by fermentation involves
 PT culturing microorganism comprising Glucosamine-6-phosphate
 PT acetyltransferase, in fermentation medium, and collecting product.
 XX
 XX Claim 15; SEQ ID NO 10; 327pp; English.
 XX
 CC The present invention relates to a method (M1) for producing glucosamine
 CC and N-acetylglucosamine by fermentation. The method comprises (a)
 CC culturing in a fermentation medium a microorganism (I) which comprises
 CC endogenous Glucosamine-6-phosphate acetyltransferase (II) and a genetic
 CC modification that increases the activity of (II), Glucosamine-6-phosphate
 CC synthase (III) or glucosamine-6-phosphate deaminase (IV), or decreases
 CC the activity of (IV) and increases the activity of Glucosamine-1-
 CC phosphate N-acetyltransferase (V), and (b) and collecting the product,
 CC which is chosen from the group consisting of Glucosamine-6-phosphate,
 CC glucosamine, glucosamine-1-phosphate, N-acetylglucosamine-1-phosphate,
 CC acetylglucosamine-6-phosphate, and N-acetylglucosamine. The present
 CC sequence was used to illustrate the method of the invention.
 XX
 SQ Sequence 609 AA;

Query Match 99.8%; Score 3080; DB 8; Length 609;
 Best Local Similarity 99.8%; Pred. No. 1.6e-263;
 Matches 608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MCGIVGAIQRDVAEILLEGRLRRLERYGDSAGLAVIDAEGMTTRLRLGKQMLAAAE 60
 Db 1 MCGIVGAIQRDVAEILLEGRLRRLERYGDSAGLAVIDAEGMTTRLRLGKQMLAAAE 60
 Qy 61 EHPLHGCTGIAHTWATHGEPSEVNAHPVSEIIVVNGIENHEPLREELKARGTYFV 120
 Db 61 EHPLHGCTGIAHTWATHGEPSEVNAHPVSEIIVVNGIENHEPLREELKARGTYFV 120
 Qy 121 SETDTEVIAHLVNLWELKQGTLREAVELAIPQRGAVTVIDMSRHDPTLLAARSQSPV 180
 Db 121 SETDTEVIAHLVNLWELKQGTLREAVELAIPQRGAVTVIDMSRHDPTLLAARSQSPV 180
 Qy 181 IGLGMGENTIASDOLALLFVTRFLFEEGDDIAETTRSVNIFDKTGAEVQRQDIESNLQ 240
 Db 181 IGLGMGENTIASDOLALLFVTRFLFEEGDDIAETTRSVNIFDKTGAEVQRQDIESNLQ 240
 Qy 241 YDAGDKGTYRHYNQKEYQPNIAKNTLTKRISHQVDLSELGPNADELSKVEHTQIQA 300
 Db 241 YDAGDKGTYRHYNQKEYQPNIAKNTLTKRISHQVDLSELGPNADELSKVEHTQIQA 300
 Qy 301 CGTSYNSGMVSYRWFESLAGIIPDVEIAESFRYRKSAVRNSLMTISQSGETADPLAGL 360
 Db 301 CGTSYNSGMVSYRWFESLAGIIPDVEIAESFRYRKSAVRNSLMTISQSGETADPLAGL 360
 Qy 361 RLSELGLTGSLSLAICNVPSSSLYRESDLALMTNAGTEIGVASTKRAFTQTLVLLMVLAKL 420
 Db 361 RLSELGLTGSLSLAICNVPSSSLYRESDLALMTNAGTEIGVASTKRAFTQTLVLLMVLAKL 420
 Qy 422 SRLKGIDASIEHDIVHGLQALPSRIEQMISODKRIEALADEFSDKHHALFLGRGDQYPIA 480
 Db 421 SRLKGIDASIEHDIVHGLQALPSRIEQMISODKRIEALADEFSDKHHALFLGRGDQYPIA 480
 Qy 481 LEGALKLKEISYTHAAYAAGELKHGPPLAIDAMPVYVARNELLEKLSNIEVRAR 540
 Db 481 LEGALKLKEISYTHAAYAAGELKHGPPLAIDAMPVYVARNELLEKLSNIEVRAR 540
 Qy 541 GGOLYVFAODQAGEVSSDMHIIEMPHVEVIAPIFYVPLQLLAYVALIKGTVDQPR 600
 Db 541 GGQIYVFAODQAGEVSSDMHIIEMPHVEVIAPIFYVPLQLLAYVALIKGTVDQPR 600
 Qy 601 NLAKSVTVE 609
 Db 601 NLAKSVTVE 609

Db	421	SRLKGIDASIEHDIVHGLQALPSRIEQMQLSDQKIREALLAEDFSDKHHAFLSLRGDQYPPA	480	
Qy	481	LEGALIKKEISYIHAAYAAGELKHGPLAIIADMPVIVAPPNELLCKNSNIEEVRAR	540	
Db	481	LEGALIKKEISYIHAAYAAGELKHGPLAIIADMPVIVAPPNELLCKNSNIEEVRAR	540	
Qy	541	GGOLYVFAODDAGYFSSDNHHTIEMPVVERIAPIFTYPLQLIAYHVALIKGTDVQPR	600	
Db	541	GGOLYVFAODDAGYFSSDNHHTIEMPVVERIAPIFTYPLQLIAYHVALIKGTDVQPR	600	
Qy	601	NLAKSYTVE	609	
Db	601	NLAKSYTVE	609	
		RESULT 11		
AC	AD138867	AD138867 standard; protein; 609 AA.		
XX				
XX	15-APR-2004	(first entry)		
XX	DT	Mutant glucosamine-6-phosphate synthase.	SEQ ID 12.	
DB				
XX				
Glucosamine; N-acetylglucosamine; fermentation;				
glucosamine-6-phosphate acetyltransferase;				
KW glucosamine-6-phosphate synthase; glucosamine-6-phosphate deaminase;				
KW glucosamine-1-phosphate N-acetyltransferase; glucosamine-6-phosphate;				
KW N-acetylglucosamine-1-phosphate; enzyme.				
Escherichia coli.				
OS Synthetic.				
XX				
XX	WO200403175-A2.			
XX	08-JAN-2004.			
XX	01-JUL-2003; 20031NO-US020925.			
XX	01-JUL-2002; 2002US-0393348P.			
XX	08-JAN-2004.			
PA (ARKI -) ARKION LIFE SCI LLC.				
XX				
PI Deng M, Angerer JD, Grund AD, Jerrell TA, Leanna C;				
PI Mathre O, Rossen R, Running J, Severson D, Song L, Wassink S;				
XX				
WPI; 2004-203380/19.				
DR N-PSDB; AD138866.				
XX				
Producing glucosamine or N-acetylglucosamine by fermentation involves				
culturing microorganism comprising glucosamine-6-phosphate acetyltransferase, in fermentation medium, and collecting product.				
XX				
Claim 15; SEQ ID NO 12; 327pp; English.				
XX				
PT Producing glucosamine or N-acetylglucosamine by fermentation involves				
PT culturing microorganism comprising glucosamine-6-phosphate acetyltransferase, in fermentation medium, and collecting product.				
XX				
PS 2004-203380/19.				
DR				
XX				
Producing glucosamine or N-acetylglucosamine by fermentation involves				
culturing microorganism comprising glucosamine-6-phosphate acetyltransferase, in fermentation medium, and collecting product.				
XX				
CC The present invention relates to a method (M1) for producing glucosamine and N-acetylglucosamine by fermentation.				
CC culturing in a fermentation medium a microorganism (I) which comprises				
CC endogenous glucosamine-6-phosphate acetyltransferase (II) and a genetic				
CC modification that increases the activity of (II), glucosamine-6-phosphate				
CC synthase (III) or glucosamine-6-phosphate deaminase (IV), or decreases				
CC the activity of (IV) and increases the activity of glucosamine-1-				
CC phosphate N-acetyltransferase (V), and (b) and collecting the product,				
CC which is chosen from the group consisting of glucosamine-6-phosphate,				
CC glucosamine, glucosamine-1-phosphate, N-acetylglucosamine-1-phosphate,				
CC acetylglucosamine-6-phosphate, and N-acetylglucosamine. The present				
CC sequence was used to illustrate the method of the invention.				
XX				
Sequence 609 AA;				
Query Match				
	99.8%; Score 3080; DB 8; Length 609;			

Best Local Similarity	99.8%; Pred. No. 1.6e-263;
Matches	608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy	1 MCGTGAIAQDVAILEGLSLRRLREYRGYDAGLAVDAGLAEGHMTRLRLRGKQVMAQRAE 60
Db	1 MCGTGAIAQDVAILEGLSLRRLREYRGYDAGLAVDAGLAEGHMTRLRLRGKQVMAQRAE 60
Qy	61 EHPPLGGTGAHTKWAATHGEPESEVNAHPHYSIETVUVVANGIIEFNEHPLRPLBKLARGYTFV 120
Db	61 EHPPLGGTGAHTKWAATHGEPESEVNAHPHYSIETVUVVANGIIEFNEHPLRPLBKLARGYTFV 120
Qy	121 SETDTEVIAHLVNWELKQGTLRBAVLRAIPQRLGAYGTIVMDSRHPDTLAAARGSPVLV 180
Db	121 SETDTEVIAHLVNWELKQGTLRBAVLRAIPQRLGAYGTIVMDSRHPDTLAAARGSPVLV 180
Qy	181 IGLGAGENFTASDQALLEPVTRRFLFLEFGDIAETTRRSVNIFDTGAEVTRQDIESNLQ 240
Db	181 IGLGAGENFTASDQALLEPVTRRFLFLEFGDIAETTRRSVNIFDTGAEVTRQDIESNLQ 240
Qy	241 YDAGPKGTYRHYMOKEIYQPNIAKNTLGRISHQVDSLSEGPNADELLSKVHIIQILA 300
Db	241 YDAGPKGTYRHYMOKEIYQPNIAKNTLGRISHQVDSLSEGPNADELLSKVHIIQILA 300
Qy	301 CGTSYNSGMVSRWYFESLAGIPCDVIAESEFRKSAVRRNSLMTLSOSGETADTLAGL 360
Db	301 CGTSYNSGMVSRWYFESLAGIPCDVIAESEFRKSAVRRNSLMTLSOSGETADTLAGL 360
Qy	361 RLSKELGYLGSLATCNPVSSLYVRESDLALMTNAGTEIGVASTKAFFTTOLTVLMLVAKL 420
Db	361 RLSKELGYLGSLATCNPVSSLYVRESDLALMTNAGTEIGVASTKAFFTTOLTVLMLVAKL 420
Qy	421 SRLKGDLASIEHDIVHGLQALPSRIEQMQLSDQKIREALLAEDFSDKHHAFLSLRGDQYPPA 480
Db	421 SRLKGDLASIEHDIVHGLQALPSRIEQMQLSDQKIREALLAEDFSDKHHAFLSLRGDQYPPA 480
Qy	481 LEGALKLKBEISYTHAEAYAEGELKGPLALIDADMPVIVAPNNELEKUKSNTEEVRAR 540
Db	481 LEGALKLKBEISYTHAEAYAEGELKGPLALIDADMPVIVAPNNELEKUKSNTEEVRAR 540
Qy	541 GGQIYVFAQDAGYFSSDNHITEMPHYEVIAPIFYTPQLOIAYHVALIKGTDVDQPR 600
Db	541 GGQIYVFAQDAGYFSSDNHITEMPHYEVIAPIFYTPQLOIAYHVALIKGTDVDQPR 600
Qy	601 NLAKSYTVE 609
Db	601 NLAKSYTVE 609

RESULT 12

AAY58825 standard; protein; 609 AA.

ID AAY58825

AA58825;

XX DT 08-MAY-2000 (first entry)

DE B. coli glucosamine-6-phosphate synthase mutant GlcN6P-S-124.

XX KW Glucosamine-6-phosphate synthase; mutant; GlcN6P-S-124;

XX KW glucosamine; metabolic engineering; plasmid pKLN23-124; mutein.

XX OS Escherichia coli.

XX Key Location/Qualifiers

XX FT Misc-difference 469

XX FT /note= "replaces wild-type Leu"

XX PN WO200004182-A1.

XX XX

XX PD 27-JAN-2000.

XX PF 15-JUL-1999;

XX XX 99W0-US015976.

XX XX

PR 15-JUL-1998;	98US-00115475.	Qy 601 NLAKSTVTE 609
XX (DCVB-) DCV INC DBA BIO-TECH RESOURCES.		Db 601 NLAKSTVTE 609
XX PI Berry A, Burlingame RP, Millis JR;		
XX DR N-PSDB; AA258252.		
XX PT Fermentation of <i>E. coli</i> having an altered amino acid sugar metabolic pathway to produce glucosamine, especially using novel recombinant variant glucosamine-6-phosphate synthases.		RESULT 13 ID ADI38863 standard; protein; 609 AA.
XX PT WPI; 2000-182441/16.		XX
XX DR ADI38863;		AC
XX DT 15-APR-2004 (first entry)		XX
PS XX		DE Mutant glucosamine-6-phosphate synthase, glms*124, SEQ ID 8.
PS XX		KW Glucosamine; N-acetylglucosamine; fermentation;
PS XX		KW glucosamine-6-phosphate acetyltransferase;
PS XX		KW glucosamine-6-phosphate synthase; glucosamine-6-phosphate deaminase;
PS XX		KW glucosamine-1-phosphate; N-acetylglucosamine-6-phosphate; glucosamine-1-phosphate;
PS XX		KW glucosamine-1-phosphate; N-acetylglucosamine-6-phosphate; enzyme.
PS XX		XX Escherichia coli.
PS XX		OS Synthetic.
PS XX		PN WO200403175-A2.
PS XX		XX
PS XX		PD 08-JAN-2004.
PS XX		XX
PS XX		PP 01-JUL-2003; 2003WO-US020925.
PS XX		PP 01-JUL-2002; 2002US-0393348P.
Qy 1 MCGIVGAIQDVAEILGLRRLYRGDSAGLAVDAEIGMTRIQLRKYQMLAQAE 60		XX PA (ARK-) ARKION LIFE SCI LLC.
Db 1 MCGIVGAIQDVAEILGLRRLYRGDSAGLAVDAEIGMTRIQLRKYQMLAQAE 60		XX PI Deng M, Angerer JD, Cyron D, Grund AD, Jerrell TA, Leanna C, Wassink S;
Qy 61 EPHLHGTTGTAHTMATHGEPESEYNAHPVSEHIVVHNGIENHEPLREELKARGYTFV 120		PI Matthe O, Robson R, Running J, Severson D, Song L;
Db 61 EPHLHGTTGTAHTMATHGEPESEYNAHPVSEHIVVHNGIENHEPLREELKARGYTFV 120		XX DR WPI: 2004-203180/19.
Db 121 SETDTEVIAHLVNLWBLKQGTLLREAVRLAIPOLRGAYGTIVMDSRHDPTLLAARSGPLV 180		XX DR N-PSDB; ADI38862.
Qy 121 SETDTEVIAHLVNLWBLKQGTLLREAVRLAIPOLRGAYGTIVMDSRHDPTLLAARSGPLV 180		PT Producing glucosamine or N-acetylglucosamine by fermentation involves culturing microorganism comprising glucosamine-6-phosphate acetyltransferase, in fermentation medium, and collecting product.
Db 121 SETDTEVIAHLVNLWBLKQGTLLREAVRLAIPOLRGAYGTIVMDSRHDPTLLAARSGPLV 180		XX PS Claim 15; SEQ ID NO 8; 327pp; English.
Qy 181 IGLGENGENTASDQLLIPVTRTEFLFEGDIAEITRSVNIFDKTGAEVQRQDIESNLQ 240		XX CC The present invention relates to a method (M1) for producing glucosamine and N-acetylglucosamine by fermentation. The method comprises (a) culturing in a fermentation medium a microorganism (I) which comprises endogenous glucosamine-6-phosphate acetyltransferase (II) and a generic modification that increases the activity of (II), glucosamine-6-phosphate synthase (III) or glucosamine-6-phosphate deaminase (IV), or decreases the activity of (IV) and increases the activity of glucosamine-1-phosphate N-acetyltransferase (V), and (b) collecting the product, which is chosen from the group consisting of glucosamine-6-phosphate, glucosamine, glucosamine-1-phosphate, N-acetylglucosamine-1-phosphate, N-acetylglucosamine-6-phosphate, and N-acetylglucosamine. The present sequence was used to illustrate the method of the invention.
Db 181 IGLGENGENTASDQLLIPVTRTEFLFEGDIAEITRSVNIFDKTGAEVQRQDIESNLQ 240		XX CC
Qy 241 YDAGDKGTYRHNMQEKEYQNAIKNTLGRISHGQVDSLSEGPNADELLSKVHENQIQLA 300		CC CC
Db 241 YDAGDKGTYRHNMQEKEYQNAIKNTLGRISHGQVDSLSEGPNADELLSKVHENQIQLA 300		CC CC
Qy 301 CGTTSYNSGMVSRWYFESLGIQPCDVEASFRYRSAVRSLMITSQSGSETADTLAGL 360		CC CC
Db 301 CGTTSYNSGMVSRWYFESLGIQPCDVEASFRYRSAVRSLMITSQSGSETADTLAGL 360		CC CC
Qy 361 RLSEKLGTLGTSLATCNVPGSSLVRESIDALMNAETGIVASTKATTQTLVLMVAKL 420		CC CC
Db 361 RLSEKLGTLGTSLATCNVPGSSLVRESIDALMNAETGIVASTKATTQTLVLMVAKL 420		XX CC
Qy 421 SRLKGLDASIEHDIVHGLQALPSRTEQMLSDQKRITALAEDFSDGKHALFGRQDQYPIA 480		XX XX Sequence 609 AA;
Db 421 SRLKGLDASIEHDIVHGLQALPSRTEQMLSDQKRITALAEDFSDGKHALFGRQDQYPIA 480		Query Match 99.8%; Score 3079; DB 8; Length 609;
Qy 481 LEGALKLKEISYTHAEAYAAGELKHGPLAIDADMPVIVAPNNELEKUKSNTIEBVR 540		Best Local Similarity 99.8%; Pred. No. 2e-263; Indels 0; Gaps 0;
Db 481 LEGALKLKEISYTHAEAYAAGELKHGPLAIDADMPVIVAPNNELEKUKSNTIEBVR 540		1 MCGIVGAIQDVAEILGLRRLYRGDSAGLAVDAEIGMTRIQLRKYQMLAQAE 60
Qy 541 GGQLYVFAQDAGFVSSDNMHIELMPFVEVIAPIFYTVPIQLLAVHVALIKGTDVDQPR 600		1 MCGIVGAIQDVAEILGLRRLYRGDSAGLAVDAEIGMTRIQLRKYQMLAQAE 60
Db 541 GGQLYVFAQDAGFVSSDNMHIELMPFVEVIAPIFYTVPIQLLAVHVALIKGTDVDQPR 600		61 EPHLHGTTGTAHTMATHGEPESEVNAHPVSEHIVVHNGIENHEPLREELKARGYTFV 120
Qy 61 EPHLHGTTGTAHTMATHGEPESEVNAHPVSEHIVVHNGIENHEPLREELKARGYTFV 120		61 EPHLHGTTGTAHTMATHGEPESEVNAHPVSEHIVVHNGIENHEPLREELKARGYTFV 120

Qy	121	SETDTEVIAHLVNWELKQCGTLRRAVLRAIPQLRGAYTVIMDSRHPDTLAAARGSPV	180	DR WPI; 2000-182441/16.
Db	121	SETDTEVIAHLVNWELKQCGTLRRAVLRAIPQLRGAYTVIMDSRHPDTLAAARGSPV	180	XX N-PSDB; AAZ58250.
Qy	181	IGLGMGENTIASDQLLLPVTRRFPLFEGDIAITRRSVNIFDKTGAEVKRDIESNLQ	240	XX Fermentation of <i>E. coli</i> having an altered amino acid sugar metabolic pathway to produce glucosamine, especially using novel recombinant variant glucosamine-6-phosphate synthases.
Db	181	IGLGMGENTIASDQLLLPVTRRFPLFEGDIAITRRSVNIFDKTGAEVKRDIESNLQ	240	XX
Qy	241	YDAGDKGTYRHMOKEIYQPNAAKNTLUGRISHQVDLSELGPNADELLSKYHQLA	300	XX Claim 28; Page 117-119; 150pp; English.
Db	241	YDAGDKGTYRHMOKEIYQPNAAKNTLUGRISHQVDLSELGPNADELLSKYHQLA	300	XX
Qy	301	CGTTSYNSGIVSRWPSRYWESPLAGIPCDVEIAFBFRYRKSAAVRNSLMTLSQSGEFTADTLAGL	360	CC The present sequence is that of a mutant, denoted GlcN6P-S-49, of the glucosamine-6-phosphate synthase (GlcN6P synthase) of <i>Escherichia coli</i> . When compared with the wild-type sequence (see AAY5822), the mutant includes I4T, I22T and S45P amino acid substitutions. These alterations are predicted from the mutated glnS gene in Plasmid pKLN23-49 (see AAZ58250). The invention provides methods for the overproduction of glucosamine by fermentation using a genetically engineered microorganism, especially <i>E. coli</i> , that includes a modified GlcN6P synthase. Production of the glucosamine by recombinant strain 2123-49 (pKLN23-49) was significantly increased when compared to a strain expressing wild-type GlcN6P synthase owing to reduced product inhibition
Db	301	CGTTSYNSGIVSRWPSRYWESPLAGIPCDVEIAFBFRYRKSAAVRNSLMTLSQSGEFTADTLAGL	360	XX
Qy	361	RLSKELGYGSLSAICNVPGSSLYRESDLIPFESPLAGIPCDVEIAFBFRYRKSAAVRNSLMTLSQSGEFTADTLAGL	420	CC
Db	361	RLSKELGYGSLSAICNVPGSSLYRESDLIPFESPLAGIPCDVEIAFBFRYRKSAAVRNSLMTLSQSGEFTADTLAGL	420	CC
Qy	421	SRUKGLDAIEHDIVHGLQALPSIEQMSQDKRIEALEDFSDKHHALFLGRGDQPIA	480	CC
Db	422	SRUKGLDAIEHDIVHGLQALPSIEQMSQDKRIEALEDFSDKHHALFLGRGDQPIA	480	CC
Qy	481	LEGALKLKEISYTHAEAYAAGELKHGPLLADMPVTVAPNELLKLNKSNIEVRAA	540	CC
Db	481	LEGALKLKEISYTHAEAYAAGELKHGPLLADMPVTVAPNELLKLNKSNIEVRAA	540	CC
Qy	541	GGQLYVFAQDQAGFVSSDNMHI1EMPHYEVIAPIFYTYPLQJAYHVALIKSTDVDPQR	600	CC
Db	541	GGQLYVFAQDQAGFVSSDNMHI1EMPHYEVIAPIFYTYPLQJAYHVALIKSTDVDPQR	600	CC
Qy	601	NLAKSVTVE	609	CC
Db	601	NLAKSVTVE	609	CC
RESULT 14				
AY58823				
ID		AAV58823 standard; protein; 609 AA.		
XX				
AC		AY58823;		
XX				
DT	08-MAY-2000	(first entry)		
XX				
DB		<i>E. coli</i> glucosamine-6-phosphate synthase mutant GlcN6P-S-49.		
XX				
KW		Glucosamine-6-phosphate synthase; glnS gene; mutant; GlcN6P-S-49; glucosamine; metabolic engineering; plasmid pKLN23-49; mutein.		
XX				
OS		<i>Escherichia coli</i> .		
XX				
Key		Location/Qualifiers		
Misc-difference	4	/note= "replaces wild-type Ile"		
FT				
FT				
Misc-difference	272	/note= "replaces wild-type 272"		
FT				
Misc-difference	450	/note= "replaces wild-type Ser"		
FT				
XX				
PN	WO200001182-A1.			
XX				
PD	27-JAN-2000.			
XX				
PR	15-JUL-1999;	99WO-US015976.		
XX				
PA	(DCVB-)	DCV INC DBA BIO-TECH RESOURCES.		
XX				
PI	Berry A.	Burlingame RP, Millis JR;		
XX				
RESULT 15				
Qy	541	GGQLYVFAQDQAGFVSSDNMHI1EMPHYEVIAPIFYTYPLQJAYHVALIKSTDVDPQR	600	
Db	541	GGQLYVFAQDQAGFVSSDNMHI1EMPHYEVIAPIFYTYPLQJAYHVALIKSTDVDPQR	600	
Qy	601	NLAKSVTVE	609	
Db	601	NLAKSVTVE	609	

AD138859 standard; protein; 609 AA.
 XX AD138859;
 AC AD138859;
 XX DT 15-APR-2004 (First entry)
 XX DE Mutant glucosamine-6-phosphate synthase, gImS*49, SEQ ID 4.
 XX Glucosamine; N-acetylglucosamine; fermentation;
 KW glucosamine-6-phosphate acetyltransferase;
 KW glucosamine-1 phosphate N-acetyltransferase; glucosamine-6-phosphate deaminase;
 KW glucosamine-1 phosphate N-acetyltransferase; glucosamine-6-phosphate;
 KW N-acetylglucosamine-6-phosphate; enzyme.
 XX Escherichia coli.
 OS Synthetic.
 XX WO2004003175-A2.
 XX PD 08-JAN-2004.
 XX P01-JUL-2003; 2003WO-US0209225.
 XX P01-JUL-2002; 2002US-0393348P.
 XX PA (ARKI-) ARKION LIFE SCI LLC.
 XX Deng M, Angerer JD, Cyron D, Grund AD, Jerrell TA, Leanna C;
 PI Mathre O, Robson R, Running J, Seversen D, Song L, Wassink S;
 XX DR WPI: 2004-203380/19.
 PT Producing glucosamine or N-acetylglucosamine by fermentation involves
 PT culturing microorganism comprising glucosamine 6-phosphate
 PT acetyltransferase, in fermentation medium, and collecting product.
 XX
 PS Claim 15; SEQ ID NO 4; 327bp; English.
 XX The present invention relates to a method (M1) for producing glucosamine
 CC and N-acetylglucosamine by fermentation. The method comprises (a)
 CC culturing in a fermentation medium a microorganism (I) which comprises
 CC endogenous glucosamine-6-phosphate acetyltransferase (II) and a generic
 CC modification that increases the activity of (II), glucosamine-6-phosphate
 CC synthase (III) or glucosamine-6-phosphate deaminase (IV), or decreases
 CC the activity of (IV) and increases the activity of glucosamine-1
 CC phosphate N-acetyltransferase (V), and (b) and collecting the product,
 CC which is chosen from the group consisting of glucosamine-6-phosphate,
 CC glucosamine, glucosamine-6-phosphate, N-acetylglucosamine-1-phosphate,
 CC N-acetylglucosamine-6-phosphate, and N-acetylglucosamine. The present
 CC sequence was used to illustrate the method of the invention.
 XX
 SQ Sequence 609 AA;
 QY Query Match 99.5%; Score 3071; DB 8; Length 609;
 Best Local Similarity 99.5%; Pred. No. 1e-262;
 Matches 606; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 DB 1 MCGTVGATAQRDVAILLEGRLRLEYGDSAGLAVDAEGHMTLRLGKVMLAQAAE 60
 DB 1 MCGTVGATAQRDVAILLEGRLRLEYGDSAGLAVDAEGHMTLRLGKVMLAQAAE 60
 QY 1 EPLHGGCTGIAHTRWATGEPSEVNAHPHSEHIVVANGIENHPLREELKARYTFTV 120
 DB 61 EPLHGGCTGIAHTRWATGEPSEVNAHPHSEHIVVANGIENHPLREELKARYTFTV 120
 DB 121 SETDTEVIAHLVWELKOGTIREAVIRAPOLRAYGTVIMDSRHPDTLIAARSSPLV 180
 DB 121 SETDTEVIAHLVWELKOGTIREAVIRAPOLRAYGTVIMDSRHPDTLIAARSSPLV 180
 QY 181 IGLGMGENFIASDQLLPPVTRRFIFLEEGDIAETTRSVNIFDKTGAEVVRQDIESNLQ 240

Result No.	Score	Query	Match	Length	DB	ID	Description
1	30.6	100.0	609	1	XNECGM		Glutamine-fructose hypothetical prote
2	30.8	99.9	609	2	H86058		hypothetical prote
3	30.7	99.6	609	2	G91212		Glutamine-fructose
4	30.3	98.9	609	2	AB0955		Glutamine-fructose
5	26.8	86.9	609	2	AB0500		Glutamine-fructose
6	22.7	73.6	610	2	D64067		Glutamine-fructose
7	22.6	73.4	610	2	E82316		Glutamine-fructose
8	19.9	64.6	611	2	F82951		Glutamine-fructose
9	18.6	60.5	621	2	A84933		Glutamine-fructose
10	17.0	55.2	635	2	E71272		Glutamine-fructose
11	16.9	54.9	609	2	A82844		Glutamine-fructose
12	15.9	51.7	611	2	T45493		Glutamine-fructose
13	15.7	50.9	612	2	H82032		Glutamine-fructose
14	15.6	50.8	612	2	B81246		Glutamine-fructose
15	14.9	47.0	612	2	AD3535		Glutamine-fructose
16	14.3	46.5	608	2	B95322		NodM Glutamine ami
17	14.2	46.3	608	2	C97575		Glutamine-fructose
18	14.2	46.3	608	2	AC2796		hypothetical prote
19	14.1	45.7	604	2	S69793		Glutamine-fructose
20	13.7	44.4	606	2	A75536		Glutamine-fructose
21	13.6	44.4	592	1	D70327		Glutamine-fructose
22	13.0	43.5	608	1	S01040		Glutamine-fructose
23	13.3	43.4	605	2	S16561		Glutamine-fructose
24	13.3	43.3	606	2	E87263		Glutamine-fructose
25	13.2	43.0	598	2	F75212		hypothetical prote
26	13.1	42.6	606	2	B72412		Glutamine-fructose
27	12.9	42.0	608	2	C9619		Glutamine-fructose
28	12.9	41.9	615	2	T35569		Glutamine-fructose
29	12.9	41.9	601	2	D71248		Glutamine-fructose

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OM protein - protein search, using SW model.	
Run on: August 7, 2006, 09:25:03 ; Search time 25 Seconds	(without alignments)
Title: US-10-612-779-2	2343.840 Million cell updates/sec
Perfect score: 3086	
Sequence: 1 MCIGTGAIAORDVABILLEG.....LIKGTDVDOPRNLAKSVTVE 609	
Scoring table: BLOSUM62	
Scoring table: Gapext 0.5	
Searched: 283416 seqs, 96216763 residues	
Total number of hits satisfying chosen parameters:	283416
Minimum DB seq length: 0	
Maximum DB seq length: 20000000000	
Post-processing: Minimum Match 0%	
Maximum Match 100%	
Database : Listing First 45 summaries	
Database : PIR 80.0:	
1: pi1:*	
2: pi2:*	
3: pi3:*	
4: pi4:*	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	30.6	100.0	609	1	XNECGM		Glutamine-fructose hypothetical prote
2	30.8	99.9	609	2	H86058		hypothetical prote
3	30.7	99.6	609	2	G91212		Glutamine-fructose
4	30.3	98.9	609	2	AB0955		Glutamine-fructose
5	26.8	86.9	609	2	AB0500		Glutamine-fructose
6	22.7	73.6	610	2	D64067		Glutamine-fructose
7	22.6	73.4	610	2	E82316		Glutamine-fructose
8	19.9	64.6	611	2	F82951		Glutamine-fructose
9	18.6	60.5	621	2	A84933		Glutamine-fructose
10	17.0	55.2	635	2	E71272		Glutamine-fructose
11	16.9	54.9	609	2	A82844		Glutamine-fructose
12	15.9	51.7	611	2	T45493		Glutamine-fructose
13	15.7	50.9	612	2	H82032		Glutamine-fructose
14	15.6	50.8	612	2	B81246		Glutamine-fructose
15	14.9	47.0	612	2	AD3535		Glutamine-fructose
16	14.3	46.5	608	2	B95322		NodM Glutamine ami
17	14.2	46.3	608	2	C97575		Glutamine-fructose
18	14.2	46.3	608	2	AC2796		hypothetical prote
19	14.1	45.7	604	2	S69793		Glutamine-fructose
20	13.7	44.4	606	2	A75536		Glutamine-fructose
21	13.6	44.4	592	1	D70327		Glutamine-fructose
22	13.0	43.5	608	1	S01040		Glutamine-fructose
23	13.3	43.4	605	2	S16561		Glutamine-fructose
24	13.3	43.3	606	2	E87263		Glutamine-fructose
25	13.2	43.0	598	2	F75212		hypothetical prote
26	13.1	42.6	606	2	B72412		Glutamine-fructose
27	12.9	42.0	608	2	C9619		Glutamine-fructose
28	12.9	41.9	615	2	T35569		Glutamine-fructose
29	12.9	41.9	601	2	D71248		Glutamine-fructose

Total number of hits satisfying chosen parameters:

283416

RESULT 1

XNECGM	
Glutamine-fructose-6-phosphate transaminase (isomerizing) (EC 2.6.1.16) - Escherichia coli	
N:Alternate names: glucosamine-6-phosphate isomerase (glut	
e	
C:Species: Escherichia coli	
C:Date: 31-Mar-1990 #sequence_revision 17-Oct-1997 #text_change 09-Jul-2004	
C:Accession: B65116; A30389; I41219; S17839; Q0513	
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Riley, M.; Co	
A.; Rose, D.J.; Mai, B.; Shao, Y.	
Science 277, 1453-1462, 1997	
A:Title: The complete genome sequence of Escherichia coli K-12.	
A:Reference number: A64720; MUID:97426617; PMID:9228503	
A:Status: preliminary; nucleic acid sequence not shown; translation not shown	
A:Molecule type: DNA	
A:Residues: 1-609 <BLAT>	
A:Cross-references: UNIPROT: P17169; UNIPARC: UPI0000153CA3; GB:AE000450; PMID:900096; NID:91	
A:Experimental source: strain K-12, substrain MG1655	
A:Title: Sequence requirements of Escherichia coli attM17, a specific site of transposon	
A:Reference number: I41219; MUID: 68086894; PMID:2826397	
A:Accession: A30389	
A:Molecule type: DNA	
A:Residues: 1-418, 'N', 421-609 <WAL>	
A:Cross-references: UNIPARC: UPI000016F5F4; GB:X01631; PID:943256; PID:943257; R:McKown, R.L.; Orle, K.A.; Chen, T.; Craig, N.L.	
R: Bacteriol. 170, 352-358, 1988	
A:Title: Sequence requirements of Escherichia coli attM17, a specific site of transposon	
A:Reference number: I41219; MUID: 597-609 <RES>	
A:Accession: A30389	
A:Molecule type: DNA	
A:Residues: 1-418, 'N', 421-609 <RES>	
A:Cross-references: UNIPARC: UPI000016F18D; GB:M18980; PMID:9146074; PID:91	
R:Golinelli-Pimpaneau, B.; Badet, B.	
Eur. J. Biochem. 201, 175-182, 1991	
A:Title: Possible involvement of Lyse603 from Escherichia coli glucosamine-6-phosphate by	
A:Reference number: S17839; MUID: 92007872; PMID:1915361	
A:Accession: S17839	
A:Molecule type: protein	
A:Residues: 49-50, 'X', 52-53; 218-219, 220-223, 'X', 225-231; 489-493; 504-508, 'K'; 'K'; '601-609	
A:Cross-references: UNIPARC: UPI000011EBBE; UNIPARC:UPI000011EBCE; 4A7	
C:Genetics:	
A:Map position: 4 min	
C:Function:	
A:Pathway: Glucosamine biosynthesis	
A:Note: Glucosamine-6 phosphate is used in the biosynthesis of amino sugars of asparagine	

C;Superfamily: glutamine-fructose-6-phosphate aminotransferase (isomerizing) C;Keywords: aminotransferase; isomerase E;2/609/Produkt: glutamine-fructose-6-phosphate transaminase (isomerizing) F;2/Active site: Cys #Status predicted	C;Superfamily: glutamine-fructose-6-phosphate aminotransferase (isomerizing)
Query Match 100.0%; Score 3086; DB 1; Length 609; Best Local Similarity 100.0%; Pred. No. 2e-191; Mismatches 0; Indels 0; Gaps 0; Matches 609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Query Match 99.9%; Score 3082; DB 2; Length 609; Best Local Similarity 99.8%; Pred. No. 3.7e-191; Mismatches 1; Indels 0; Gaps 0; Matches 608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MCGIVGAIQRDVAELLEGRLRLEYRGDSAGLAVDAGEMTRLRLGKVQMLQAAE 60 Db 1 MCGIVGAIQRDVAELLEGRLRLEYRGDSAGLAVDAGEMTRLRLGKVQMLQAAE 60	Qy 1 MCGIVGAIQRDVAELLEGRLRLEYRGDSAGLAVDAGEMTRLRLGKVQMLQAAE 60 Db 1 MCGIVGAIQRDVAELLEGRLRLEYRGDSAGLAVDAGEMTRLRLGKVQMLQAAE 60
Qy 61 EPHLHGCTGIAHTRWATHGEPESEVNAHPHSEHIVVHNGTIEHNPRLREELKARGTYFV 120 Db 61 EPHLHGCTGIAHTRWATHGEPESEVNAHPHSEHIVVHNGTIEHNPRLREELKARGTYFV 120	Qy 61 EPHLHGCTGIAHTRWATHGEPESEVNAHPHSEHIVVHNGTIEHNPRLREELKARGTYFV 120 Db 61 EPHLHGCTGIAHTRWATHGEPESEVNAHPHSEHIVVHNGTIEHNPRLREELKARGTYFV 120
Qy 121 SETDTEVIAHLVNLWELKOGGTIREAVLAIPOLRGAYCTVIMDSRHPDTLIAARSGSPLV 180 Db 121 SETDTEVIAHLVNLWELKOGGTIREAVLAIPOLRGAYCTVIMDSRHPDTLIAARSGSPLV 180	Qy 121 SETDTEVIAHLVNLWELKOGGTIREAVLAIPOLRGAYCTVIMDSRHPDTLIAARSGSPLV 180 Db 121 SETDTEVIAHLVNLWELKOGGTIREAVLAIPOLRGAYCTVIMDSRHPDTLIAARSGSPLV 180
Qy 181 IGLGMGENTASDQLLPLFTRTFLFLEGDLIEITRSVNFIDKTAGEVKRODIESNLQ 240 Db 181 IGLGMGENTASDQLLPLFTRTFLFLEGDLIEITRSVNFIDKTAGEVKRODIESNLQ 240	Qy 181 IGLGMENFASDQLLPLFTRTFLFLEGDLIEITRSVNFIDKTAGEVKRODIESNLQ 240 Db 181 IGLGMENFASDQLLPLFTRTFLFLEGDLIEITRSVNFIDKTAGEVKRODIESNLQ 240
Qy 241 YDAGDKGYRHYMOKEIYQPNAIKNTLGRISHGQVDSELGPNAIDELLSKVEHIIQILA 300 Db 241 YDAGDKGYRHYMOKEIYQPNAIKNTLGRISHGQVDSELGPNAIDELLSKVEHIIQILA 300	Qy 241 YDAGDKGYRHYMOKEIYQPNAIKNTLGRISHGQVDSELGPNAIDELLSKVEHIIQILA 300 Db 241 YDAGDKGYRHYMOKEIYQPNAIKNTLGRISHGQVDSELGPNAIDELLSKVEHIIQILA 300
Qy 301 CGTSYNSGMVSRYFWEFLAGIPCDVEASEFTRYSKAVRNSLMITLQSGETADTLAGL 360 Db 301 CGTSYNSGMVSRYFWEFLAGIPCDVEASEFTRYSKAVRNSLMITLQSGETADTLAGL 360	Qy 301 CGTSYNSGMVSRYFWEFLAGIPCDVEASEFTRYSKAVRNSLMITLQSGETADTLAGL 360 Db 301 CGTSYNSGMVSRYFWEFLAGIPCDVEASEFTRYSKAVRNSLMITLQSGETADTLAGL 360
Qy 361 RLSKELGYLGSIAICNPGSSLVRESDLALMTNAGTEIVGASTKAKFTTQTVLMLYAKL 420 Db 361 RLSKELGYLGSIAICNPGSSLVRESDLALMTNAGTEIVGASTKAKFTTQTVLMLYAKL 420	Qy 361 RLSKELGYLGSIAICNPGSSLVRESDLALMTNAGTEIVGASTKAKFTTQTVLMLYAKL 420 Db 361 RLSKELGYLGSIAICNPGSSLVRESDLALMTNAGTEIVGASTKAKFTTQTVLMLYAKL 420
Qy 421 SRLKGLDASIEHDIVHGLQALPRIONLSDKRIEALADSDKHALFLGRGDQYPIA 480 Db 421 SRLKGLDASIEHDIVHGLQALPRIONLSDKRIEALADSDKHALFLGRGDQYPIA 480	Qy 421 SRLKGIDASIEHDIVHGLQALPRIONLSDKRIEALADSDKHALFLGRGDQYPIA 480 Db 421 SRLKGIDASIEHDIVHGLQALPRIONLSDKRIEALADSDKHALFLGRGDQYPIA 480
Qy 481 LEGALKKEISYIHAAYAAGELKQHPLALDAMPVTVAPNNELEKLSNIEEVRAR 540 Db 481 LEGALKKEISYIHAAYAAGELKQHPLALDAMPVTVAPNNELEKLSNIEEVRAR 540	Qy 481 LEGALKKEISYIHAAYAAGELKQHPLALDAMPVTVAPNNELEKLSNIEEVRAR 540 Db 481 LEGALKKEISYIHAAYAAGELKQHPLALDAMPVTVAPNNELEKLSNIEEVRAR 540
Qy 541 GGQLYVFAQQDAGFVSSDNMHITEMPHVEVIAPIFTVPLQLAYHVALIKGTVDQPR 600 Db 541 GGQLYVFAQQDAGFVSSDNMHITEMPHVEVIAPIFTVPLQLAYHVALIKGTVDQPR 600	Qy 541 GGQLYVFAQQDAGFVSSDNMHITEMPHVEVIAPIFTVPLQLAYHVALIKGTVDQPR 600 Db 541 GGQLYVFAQQDAGFVSSDNMHITEMPHVEVIAPIFTVPLQLAYHVALIKGTVDQPR 600
Qy 601 NLAKSVTVE 609 Db 601 NLAKSVTVE 609	Qy 601 NLAKSVTVE 609 Db 601 NLAKSVTVE 609
	RESULT 3
	G91212 hypothetical protein EC84671 [Imported] - Escherichia coli (strain O157:H7, substrain RII)
	C;Species: Escherichia coli
	C;Accession: G91212
	C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
	R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yotoyama, K.; Han, C.G., .
	Gasunara, N.; Yasunara, T.; Khara, S.; Shiba, T.; Hatori, M.; Shinagawa, H.
	C;Accession: H86058
	C;DNA Res. 8, 11-22, 2001
	R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, L.; Grotbeck, B.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
	A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genome
	A;Reference number: A99629; PMID:21156231; PMID:11258796
	A;Accession: G91212
	A;Status: preliminary
	A;Molecule type: DNA
	A;Cross-references: UNIPROT:Q8XEG2; UNIPARC:UPI000016552F; GB:BA000007; PIDN:BAE38094.1; C;Genetic:
	A;Experimental source: strain O157:H7, substrain RIMD 050952
	C;Genetic:
	A;Gene: EC84671
	C;Superfamily: glutamine-fructose-6-phosphate aminotransferase (isomerizing)
	Query Match 99.6%; Score 3075; DB 2; Length 609;

Best Local Similarity	Pred. No.	1e-190;	1e-190;	Indels	0;	Gaps	0;	Query Match	Score	3053;	DB	2;	Length	609;	
Best Local Similarity	2;	Mismatches	0;	Indels	0;	Gaps	0;	Best Local Similarity	98.5%	DB	2;	Pred. No.	2.7e-189;		
Matches	607;	Conservative	5;					Matches	600;	Conservative	5;	Mismatches	4;		
1	MCGIVGAIQRDVAEILDEGLRPLLEGRYGDASGLAVVADGAETGANTRLRLGKVQMLAQAAE	60						1	MCGIVGAIQRDVAEILDEGLRPLLEGRYGDASGLAVVADGAETGANTRLRLGKVQMLAQAAE	60					
1	MCGIVGAIQRDVAEILDEGLRPLLEGRYGDASGLAVVADGAETGANTRLRLGKVQMLAQAAE	60						1	MCGIVGAIQRDVAEILDEGLRPLLEGRYGDASGLAVVADGAETGANTRLRLGKVQMLAQAAE	60					
61	EHPLHGCGTGAHTRWATGEPSEVNAHPHSEHIVVHNGTENHEPRLREELKARGTTFV	120						61	EHPLHGCGTGAHTRWATGEPSEVNAHPHSEHIVVHNGTENHEPRLREELKARGTTFV	120					
61	EHPLHGCGTGAHTRWATGEPSEVNAHPHSEHIVVHNGTENHEPRLREELKARGTTFV	120						61	EHPLHGCGTGAHTRWATGEPSEVNAHPHSEHIVVHNGTENHEPRLREELKARGTTFV	120					
121	SETDTEVIAHLVNWELKOGGTREAVLRAIPQLRGAYTVIMSRHPPTLLAARSGSPLV	180						Qy	121	SETDTEVIAHLVNWELKOGGTREAVLRAIPQLRGAYTVIMSRHPPTLLAARSGSPLV	180				
121	SETDTEVIAHLVNWELKOGGTREAVLRAIPQLRGAYTVIMSRHPPTLLAARSGSPLV	180						Qy	121	SETDTEVIAHLVNWELKOGGTREAVLRAIPQLRGAYTVIMSRHPPTLLAARSGSPLV	180				
181	IGLGMGENFIASDQLALLPVTRRFIPLIEDGIABTTRSVNIFDKTGAEVTKRDIESNLQ	240						Qy	181	IGLGMGENFIASDQLALLPVTRRFIPLIEDGIABTTRSVNIFDKTGAEVTKRDIESNLQ	240				
181	IGLGMGENFIASDQLALLPVTRRFIPLIEDGIABTTRSVNIFDKTGAEVTKRDIESNLQ	240						Db	181	IGLGMGENFIASDQLALLPVTRRFIPLIEDGIABTTRSVNIFDKTGAEVTKRDIESNLQ	240				
241	YDAGDKSIYRHYMKQIYEQPNIAKNTLGRISHGQVDLSSELGPNADELLSKVEHIIQILA	300						Qy	241	YDAGDKSIYRHYMKQIYEQPNIAKNTLGRISHGQVDLSSELGPNADELLSKVEHIIQILA	300				
241	YDAGDKSIYRHYMKQIYEQPNIAKNTLGRISHGQVDLSSELGPNADELLSKVEHIIQILA	300						Db	241	YDAGDKSIYRHYMKQIYEQPNIAKNTLGRISHGQVDLSSELGPNADELLSKVEHIIQILA	300				
301	CGTTSYNSGMVSYWFEISLAGIPCDVEIASEFPRYKSAVRENSLMTLSQSGETADTLAGL	360						Qy	301	CGTTSYNSGMVSYWFEISLAGIPCDVEIASEFPRYKSAVRENSLMTLSQSGETADTLAGL	360				
301	CGTTSYNSGMVSYWFEISLAGIPCDVEIASEFPRYKSAVRENSLMTLSQSGETADTLAGL	360						Db	301	CGTTSYNSGMVSYWFEISLAGIPCDVEIASEFPRYKSAVRENSLMTLSQSGETADTLAGL	360				
361	RLSKELGYGLGSIAICNYPGSIVRESDLALMNTNAGTEGVASTKRAFTTQLTVMLVAKL	420						Qy	361	RLSKELGYGLGSIAICNYPGSIVRESDLALMNTNAGTEGVASTKRAFTTQLTVMLVAKL	420				
361	RLSKELGYGLGSIAICNYPGSIVRESDLALMNTNAGTEGVASTKRAFTTQLTVMLVAKL	420						Db	361	RLSKELGYGLGSIAICNYPGSIVRESDLALMNTNAGTEGVASTKRAFTTQLTVMLVAKL	420				
421	SRLKGLDASIEHDIVGLQALPSRQEQLMSQDKRIEALAEFSDKHALFLGRGDQPIA	480						Qy	421	SRLKGLDASIEHDIVGLQALPSRQEQLMSQDKRIEALAEFSDKHALFLGRGDQPIA	480				
421	SRLKGLDASIEHDIVGLQALPSRQEQLMSQDKRIEALAEFSDKHALFLGRGDQPIA	480						Db	421	SRLKGLDASIEHDIVGLQALPSRQEQLMSQDKRIEALAEFSDKHALFLGRGDQPIA	480				
481	LEGALKLKEISYTHAAYAAGELKGKPIALIDADMPTVVAAPNELLKEKLKNIEETYR	540						Qy	481	LEGALKLKEISYTHAAYAAGELKGKPIALIDADMPTVVAAPNELLKEKLKNIEETYR	540				
481	LEGALKLKEISYTHAAYAAGELKGKPIALIDADMPTVVAAPNELLKEKLKNIEETYR	540						Db	481	LEGALKLKEISYTHAAYAAGELKGKPIALIDADMPTVVAAPNELLKEKLKNIEETYR	540				
541	GGQLYVADQDGFSDDNMHIEMPHVEVIAPIFYTVPLQLLAYVALIKGTDVDQPR	600						Qy	541	GGQLYVADQDGFSDDNMHIEMPHVEVIAPIFYTVPLQLLAYVALIKGTDVDQPR	600				
601	NLAKSVTVE	609						Qy	601	NLAKSVTVE	609				
601	NLAKSVTVE	609						Db	601	NLAKSVTVE	609				

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RESULT 5
AB0500
  Glutamine-fructose-6-phosphate transaminase (isomerizing) (EC 2.6.1.16) [import]
  C;Species: Yersinia pestis
  C;Date: 02-Nov-2001 #text_change 09-Jul-2004
  C;Accession: AB05000
  C;Accession: AB0500
  R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prent, R.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dou, S.; E; deno-Tarraga, A.M.; Rutherford, M.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; E; Nature 413, 523-527, 2001
  A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
  A;Reference number: AB0001; MUID:214704113; PMID:11586360
  A;Accession: AB0500
  A;Accession: AB0500
  A;Status: preliminary
  A;Molecule type: DNA
  A;Residues: 1-609 <KUR>
  A;Cross-references: UNIPROT:Q8Z9S8; UNIPARC:UPI000016587A; GB:AL590842; PIDN:CA
  C;Genetics:
  A;Gene: glmS
  C;Superfamily: Glutamine-fructose-6-phosphate aminotransferase (isomerizing)
  C;Keywords: aminotransferase; isomerase
  Query Match Score 2682; DB 2; Length 609;
  Best Local Similarity 85.1%; Pred No 2.4e-165;

```

Matches	518;	Conservative	44;	Mismatches	47;	Indels	0;	Gaps	0;	Matches	441;	Conservative	73;	Mismatches	95;	Indels	1;	Gaps	1;	
Qy	1	MCGIVGAVIAQDVAEILLEGRLRLREYRGDSAGLAIVDAEGHMTRLRLRGKVQMLAQAE	60							Qy	1	MCGIVGAVIAQDVAEILLEGRLRLREYRGDSAGLAIVDAEGHMTRLRLRGKVQMLAQAE	60							
Db	1	MCGIVGAVIAQDVAEILLEGRLRLREYRGDSAGLAIVDAEGHMTRLRLRGKVQMLAQAE	60							Db	1	MCGIVGAVIAQDVAEILLEGRLRLREYRGDSAGLAIVDAEGHMTRLRLRGKVQMLAQAE	60							
61	EPHLHGCTGIAHTWATCPESEVNAHPVSEHIVVNGTIEHNPREEELKARGTYEV	120								Qy	61	EPHLHGCTGIAHTWATCPESEVNAHPVSEHIVVNGTIEHNPREEELKARGTYEV	120							
61	KQDHGCTGIAHTWATCPESEVNAHPVSEHIVVNGTIEHNPREEELKARGTYEV	120								Db	61	KQDHGCTGIAHTWATCPESEVNAHPVSEHIVVNGTIEHNPREEELKARGTYEV	120							
121	SEITDTEVIAHLVWELKQGTTREAVLRAIPIOLRGAYGTIVMDSRHPTDILAAARGSPVL	180								Qy	121	SEITDTEVIAHLVWELKQGTTREAVLRAIPIOLRGAYGTIVMDSRHPTDILAAARGSPVL	180							
121	SEITDTEVIAHLVWHEQQQGSLLEEVKRVIPOLRGAYGTIVMDSRHPTDILAAARGSPVL	180								Db	121	SEITDTEVIAHLVWHEQQQGSLLEEVKRVIPOLRGAYGTIVMDSRHPTDILAAARGSPVL	180							
181	IGLGMGENFIASDOLALLPVTRRFIFLEGDAIEITTRSVNIFDKTGAEVKQDIESNLQ	240								Qy	181	IGLGMGENFIASDOLALLPVTRRFIFLEGDAIEITTRSVNIFDKTGAEVKQDIESNLQ	240							
181	IGCGVGENFIASDOLALLPVTRRFIFLEGDAIEITTRSVNIFDKGNAIERPEIESQV	240								Db	181	IGCGVGENFIASDOLALLPVTRRFIFLEGDAIEITTRSVNIFDKGNAIERPEIESQV	240							
241	YDAGDKG1YRHYMOKETIEQPNIAKNTLTGRISHQVDLSELGPNADELLSKVHEHQIQLA	300								Qy	241	YDAGDKG1YRHYMOKETIEQPNIAKNTLTGRISHQVDLSELGPNADELLSKVHEHQIQLA	300							
241	YDAGDKG1YRHYMOKETIEQPNIAKNTLTGRISHQVDLSELGPNADELLSKVHEHQIQLA	300								Db	241	YDAGDKG1YRHYMOKETIEQPNIAKNTLTGRISHQVDLSELGPNADELLSKVHEHQIQLA	300							
301	CGTTSYNSGMVSYWFEISLAGVPCDVEIASEFRYKSAVRNSLIMLTSOSGETADTLAGL	360								Qy	301	CGTTSYNSGMVSYWFEISLAGVPCDVEIASEFRYKSAVRNSLIMLTSOSGETADTLAGL	360							
301	CGTTSYNSGMVSYWFEISLAGVPCDVEIASEFRYKSAVRNSLIMLTSOSGETADTLAGL	360								Db	301	CGTTSYNSGMVSYWFEISLAGVPCDVEIASEFRYKSAVRNSLIMLTSOSGETADTLAGL	360							
361	RLSKELGYLGSLAICNVGSSLVYRESIDLALMNTAGTEIVGASTKAFTQLTVLMLVAKL	420								Qy	361	RLSKELGYLGSLAICNVGSSLVYRESIDLALMNTAGTEIVGASTKAFTQLTVLMLVAKL	420							
361	RLSKELGYLGSLAICNVGSSLVYRESIDLALMNTAGTEIVGASTKAFTQLTVLMLVAKL	420								Db	361	RLSKELGYLGSLAICNVGSSLVYRESIDLALMNTAGTEIVGASTKAFTQLTVLMLVAKL	420							
421	SRKGLDASLEIDIVHQLQALSRQKRIEALAEEDSDKHALFLRGDQYPIA	480								Qy	421	SRKGLDASLEIDIVHQLQALSRQKRIEALAEEDSDKHALFLRGDQYPIA	480							
421	GRKGADASLEIDIVHQLQALSRQKRIEALAEEDSDKHALFLRGDQYPIA	480								Db	421	GRKGADASLEIDIVHQLQALSRQKRIEALAEEDSDKHALFLRGDQYPIA	480							
481	LEGALKLUKEISYTHAAYAAGELKHGPALIADMPVIVAPNNELELKLSNIEEYRA	540								Qy	481	LEGALKLUKEISYTHAAYAAGELKHGPALIADMPVIVAPNNELELKLSNIEEYRA	540							
481	MEGALKLUKEISYTHAAYAAGELKHGPALIADMPVIVAPNNELELKLSNIEEYRA	540								Db	481	MEGALKLUKEISYTHAAYAAGELKHGPALIADMPVIVAPNNELELKLSNIEEYRA	540							
541	GGLYWFAQDQGFVSSDNMH1EMPFEEVIAPIFYTVPLQLAYVALIKGTDVQDQP	600								Qy	540	GGLYWFAQDQGFVSSDNMH1EMPFEEVIAPIFYTVPLQLAYVALIKGTDVQDQP	599							
541	GGLYWFAQDQGFTDSEGMR1QLPVHEE1IAPIFYTVPLQLSTHVALIKGTDVQDQP	600								Db	541	GGLYWFAQDQGFTDSEGMR1QLPVHEE1IAPIFYTVPLQLSTHVALIKGTDVQDQP	600							
601	NIAKSVTVE	609								Qy	600	NIAKSVTVE	609							
601	NIAKSVTVE	609								Db	601	NIAKSVTVE	609							

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Glutamine-fructose-6-phosphate transaminase (isomerizing) (EC 2.6.1.16) - Haemophilus influenzae

#:Accession: DE405711
#:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
#:Title: *Haemophilus influenzae* Rd.

;Accession: D64067
;Status: nucleic acid sequence not shown; translation not shown
;Source: *Leptospiral*, *Leptospiral*.

Molecule type: DNA
Residues: 1-610 <TIGR>

Cross-references: UNIPROT:P44708; UNIPARC:UB100000512BF; GB:U32726; GB:L42023; NID:915
Note: named as homolog to a protein from *Escherichia coli*

Superfamily: glutamine-fructose-6-phosphate aminotransferase (isomerizing)
Keywords: aminotransferase; isomerase

```
#2-610/Product: glutamine-fructose-6-phosphate transaminase (isomerizing) #status predicted
#2/Active site: Cys #status predicted
```

Query Match 73.6%; Score 2270.5; DB 2; Length 610;

RESULTS 7
3823316
L-glutamine-fructose-6-phosphate transaminase (isomerizing) (EC 2.6.1.16) (similarity 0.85)
Species: *Vibrio cholerae*

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#:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
#:Accession: EPI2316
#:Organism: Vibrio cholerae
#:Strain: O139
#:Author: J.F. Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Smith, D.; Richardson, D.; Rasmussen, M.D.; Vanathavan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sealfon, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
#:Journal: Nature
#:Volume: 406
#:Page: 477-483
#:Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
#:Reference: A82035; MUID:20406833; PMID:10932301
#:Contributor: Vibrio cholerae Project, NCBI
```

Accession: 202310
A.Status: Preliminary
A.Molecule: RNA
A.Molecule: DNA

• Cross-references: UNIKU:QKUM8; UNIPARC:UP1000164853; GB:AE004135; GB:AE00385
• Experimental source: serogroup O1; strain N16961; biotype El Tor
• Genetics:

Map position: 1
Superfamily: glutamine-fructose-6-phosphate aminotransferase (isomerizing)
Keywords: aminotransferase; isomerase

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Query Match	Score	DB 2;	Length	610;	Score	1995;	DB 2;	Length	611;
Best Local Similarity	73.4%;	Pred. No.	2.e-138;		62.7%;	Pred. No.	5.4e-121;		
Matches	437;	Conservative	72;	Mismatches	100;	Indels	1;	Gaps	1;
Qy	1	MCGIVGAIQORDVAILELLERLRLRRLRLLRLLRQVQMLAQAAE	60						
Db	1	MCGIVGAIQORDVAILEVQLQRLRLRRLRLLRQVQMLQDAVE	60						
Qy	61	EPLHGGTCIAHTRWAHGPSEVNAHPHYSIETVYVHNGIENHEPLRBLKRGYTFV	120						
Db	61	AAQVAGGTGIAHTRWAHGPSEVNAHPHISGDTIVVHNGIENHEMLRMLQDRGYFV	120						
Qy	121	SETDTEVIAHLVWELKQGCTLREAVRLRPAIPOLRAYGTIVMDSRHPDTLAAARGSPLV	180						
Db	121	SQTDTEVIAHLVWELKQGCTLREAVRLRPAIPOLRAYGTIVMDRNPDRIVARSGPIV	180						
Qy	181	IGLGMGENFTASDQDALLPVTTRFLFLEEDIAETTRRSVNTFDKTAGTAEYTKRQDIESNLQ	240						
Db	181	IGLGMGENFTASDQDALLPVTTRFLFLEEDIAETTRRSVNTFDKTAGTAEYTKRQDIESNLQ	240						
Qy	241	YDAGDKGIVYRHYMKQEYEQPNAKNTLGRISHQVQDLSLGPNNADELLSKVHIIQIL	300						
Db	241	HDADKGHYRHYMKQEYEQPNAKNTLGRISHQVQDLSLGPNNADELLSKVHIIQIL	300						
Qy	301	CGTSYNSGMVRYTFESLQAGPCDVEIASFRYKSAVRNSLMTLSQGETADTLGL	360						
Db	301	CGTSYNAQTMARYTFESLQAGPCDVEIASFRYKXFKVTRENSLLTTSQGETADTLA	360						
Qy	361	RLSKELGYLGSLATCNPVGPSSLYVRESDLALMTNAGTEIGVASTKAFTTOLTVLMLVAKL	420						
Db	361	RLAKEGYMAAMTCNVAGSLVRESDFAMTRAGTEIGVASTKAFTTOLTVLMLVAKL	420						
Qy	421	SR-LKGLDAS1EHDIVHGLALPSR1EQM1SQRK1EALNEDFSKXH1FLGRDQYPI	479						
Db	421	GKQQRIGRLEAEVH1ALH1LQ101ETLAFDQKHT1FLGRGEYYP1	480						
Qy	480	ALEGALKKEISYTHAEAYAAGELKXHGPPL1ADMPVTVAPNBNELLEKLKSNT1EEVRA	539						
Db	481	AVEASLKLKEISYTHAEAYAAGELKXHGPPL1ADMPVTVAPNBNELLEKLKSNT1EEVRA	540						
Qy	540	RGGOLYVFADQGVSSDMH1EMPHYVEVIAPIFYTVPLQ1AYHVALIKETDVIDP	599						
Db	541	RGGHLYVFADVEAFEDTMK11AMPHYSEIVAPIYYTTPMQ1LSYHVALIKETDVIDP	600						
Qy	600	RNLAKSVTVE	609						
Db	601	RNLAKAVTVE	610						
Qy	610	PRNLAKSVTVE	609						
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Qy 1 MCGIVGAI-ARDVAVILLEURRLYRGDSAGLAUDDEAGMTRLRRKGKVQNLQA 59	Qy 1 MCGIVGAI-ARDVAVILLEURRLYRGDSAGLAUDDEAGMTRLRRKGKVQNLQA 59	Qy 1 MCGIVGAI-ARDVAVILLEURRLYRGDSAGLAUDDEAGMTRLRRKGKVQNLQA 59	A;Gene: NMB0031	A;Gene: NMB0031	A;Gene: NMB0031
Best Local Similarity 50.9%; Score 1570.5; DB 2; Length 612;	Best Local Similarity 50.8%; Score 1570.5; DB 2; Length 612;	Best Local Similarity 50.8%; Score 1566.5; DB 2; Length 612;	C;Supertable: Glutamine-fructose-6-phosphate aminotransferase (isomerizing)	C;Supertable: Glutamine-fructose-6-phosphate aminotransferase (isomerizing)	C;Supertable: Glutamine-fructose-6-phosphate aminotransferase (isomerizing)
Matches 325; Conservative 104; Mismatches 177; Indels 9; Gaps 9;	Matches 325; Conservative 104; Mismatches 177; Indels 9; Gaps 9;	Matches 321; Conservative 104; Mismatches 182; Indels 7; Gaps 7;	C;Keywords: aminotransferase; isomerase	C;Keywords: aminotransferase; isomerase	C;Keywords: aminotransferase; isomerase
Db 1 MCGIVGAI-ARDVAVILLEURRLYRGDSAGLAUDDEAGMTRLRRKGKVQNLQA 59	Db 1 MCGIVGAI-ARDVAVILLEURRLYRGDSAGLAUDDEAGMTRLRRKGKVQNLQA 59	Db 1 MCGIVGAI-ARDVAVILLEURRLYRGDSAGLAUDDEAGMTRLRRKGKVQNLQA 59	F;2/612/Active site: Cys #status predicted	F;2/612/Active site: Cys #status predicted	F;2/612/Active site: Cys #status predicted
Qy 60 BEHPLGGTGGAHTKWAHGPPSEVNAHPVS-EHIVVYVNGTILENHEPRLREELKARGYT 118	Qy 60 BEHPLGGTGGAHTKWAHGPPSEVNAHPVS-EHIVVYVNGTILENHEPRLREELKARGYT 118	Qy 60 BEHPLGGTGGAHTKWAHGPPSEVNAHPVS-EHIVVYVNGTILENHEPRLREELKARGYT 118	C;Supertable: aminotransferase	C;Supertable: aminotransferase	C;Supertable: aminotransferase
Db 60 REKGISGGTIGIGHTWATHSGCVTENAHNPISGMIAVNGTILENHEPRLREELKARGLT 119	Db 60 REKGISGGTIGIGHTWATHSGCVTENAHNPISGMIAVNGTILENHEPRLREELKARGLT 119	Db 60 REKGISGGTIGIGHTWATHSGCVTENAHNPISGMIAVNGTILENHEPRLREELKARGLT 119	F;2/612/Product: glutamine-fructose-6-phosphate transaminase	F;2/612/Product: glutamine-fructose-6-phosphate transaminase	F;2/612/Product: glutamine-fructose-6-phosphate transaminase
Qy 119 FVSETDTEVIAHLVNWELKQ-GGTLLREAVRAIPOLRGAYGTIVMDSRHPTDLAARSGS 177	Qy 119 FVSETDTEVIAHLVNWELKQ-GGTLLREAVRAIPOLRGAYGTIVMDSRHPTDLAARSGS 177	Qy 119 FVSETDTEVIAHLVNWELKQ-GGTLLREAVRAIPOLRGAYGTIVMDSRHPTDLAARSGS 177	A;Accession: B81246	A;Accession: B81246	A;Accession: B81246
Db 120 FESQIDTEVIAHSSINHEYANGGKLFLEAQAVERFHGAYAIAVIAQDKEPDELVARMCC 179	Db 120 FESQIDTEVIAHSSINHEYANGGKLFLEAQAVERFHGAYAIAVIAQDKEPDELVARMCC 179	Db 120 FESQIDTEVIAHSSINHEYANGGKLFLEAQAVERFHGAYAIAVIAQDKEPDELVARMCC 179	A;Status: preliminary	A;Status: preliminary	A;Status: preliminary
Qy 178 PLVIGLGMGENFIAISDQLALIPVTPRERIFLEEGDIAETRTRSV-NIFDYGAEVKRQDE 236	Qy 178 PLVIGLGMGENFIAISDQLALIPVTPRERIFLEEGDIAETRTRSV-NIFDYGAEVKRQDE 236	Qy 178 PLVIGLGMGENFIAISDQLALIPVTPRERIFLEEGDIAETRTRSV-NIFDYGAEVKRQDE 236	A;Experimental source: serogroup A, strain Z2491	A;Experimental source: serogroup A, strain Z2491	A;Experimental source: serogroup A, strain Z2491
Db 180 PLLVAGLDDETFIASDVSATIAFTRRAVLEDGTDIALASDG1KRLDKSGLPAERKVKV 239	Db 180 PLLVAGLDDETFIASDVSATIAFTRRAVLEDGTDIALASDG1KRLDKSGLPAERKVKV 239	Db 180 PLLVAGLDDETFIASDVSATIAFTRRAVLEDGTDIALASDG1KRLDKSGLPAERKVKV 239	A;Molecule type: DNA	A;Molecule type: DNA	A;Molecule type: DNA
Qy 237 SNLQVDAQDGKIGYRHYMOKEIYEQPNATKNTLGRISHQGDVLSELGPNADELLSKVHEI 296	Qy 237 SNLQVDAQDGKIGYRHYMOKEIYEQPNATKNTLGRISHQGDVLSELGPNADELLSKVHEI 296	Qy 237 SNLQVDAQDGKIGYRHYMOKEIYEQPNATKNTLGRISHQGDVLSELGPNADELLSKVHEI 296	C;Species: <i>Neisseria meningitidis</i>	C;Species: <i>Neisseria meningitidis</i>	C;Species: <i>Neisseria meningitidis</i>
Db 240 SELSASLIEGLPYSHEFWMQELHEQPNATDTEYFLDGFIP-ENFGNKAQFESTRSV 298	Db 240 SELSASLIEGLPYSHEFWMQELHEQPNATDTEYFLDGFIP-ENFGNKAQFESTRSV 298	Db 240 SELSASLIEGLPYSHEFWMQELHEQPNATDTEYFLDGFIP-ENFGNKAQFESTRSV 298	C;Accession: AD3595	C;Accession: AD3595	C;Accession: AD3595
Qy 297 QILACGTSYNSGMVNSR/TWESLAGIPDVEILSEFRKSAVRNSM/ITLSSQGETADT 356	Qy 297 QILACGTSYNSGMVNSR/TWESLAGIPDVEILSEFRKSAVRNSM/ITLSSQGETADT 356	Qy 297 QILACGTSYNSGMVNSR/TWESLAGIPDVEILSEFRKSAVRNSM/ITLSSQGETADT 356	RESULT 15	RESULT 15	RESULT 15
Db 299 KILACGTSYAAALTAKYWEISAKPSDVEIAFSPVTAQDOLVITISQGETLDT 358	Db 299 KILACGTSYAAALTAKYWEISAKPSDVEIAFSPVTAQDOLVITISQGETLDT 358	Db 299 KILACGTSYAAALTAKYWEISAKPSDVEIAFSPVTAQDOLVITISQGETLDT 358	AD3595	AD3595	AD3595
Qy 357 LAGLRLSKELGYLGSLSAICVPGSSSLVRESDLALMNTAGTIGASIAKRAFTQLVML 416	Qy 357 LAGLRLSKELGYLGSLSAICVPGSSSLVRESDLALMNTAGTIGASIAKRAFTQLVML 416	Qy 357 LAGLRLSKELGYLGSLSAICVPGSSSLVRESDLALMNTAGTIGASIAKRAFTQLVML 416	Glutamine-fructose-6-phosphate transaminase (isomerizing)	Glutamine-fructose-6-phosphate transaminase (isomerizing)	Glutamine-fructose-6-phosphate transaminase (isomerizing)
Db 359 MEALKYAKSLGHRHSLSIGVMESALPRESLVLTYTRGAETGVASTKAKFTQLVALFGL 418	Db 359 MEALKYAKSLGHRHSLSIGVMESALPRESLVLTYTRGAETGVASTKAKFTQLVALFGL 418	Db 359 MEALKYAKSLGHRHSLSIGVMESALPRESLVLTYTRGAETGVASTKAKFTQLVALFGL 418	C;Species: <i>Brucella melitensis</i>	C;Species: <i>Brucella melitensis</i>	C;Species: <i>Brucella melitensis</i>
Qy 417 VAKSLRILKQD-SASIEHDIVHGLQALPSRIBEQMQLSDQKREIALEADFSDKHHLFLGRGD 475	Qy 417 VAKSLRILKQD-SASIEHDIVHGLQALPSRIBEQMQLSDQKREIALEADFSDKHHLFLGRGD 475	Qy 417 VAKSLRILKQD-SASIEHDIVHGLQALPSRIBEQMQLSDQKREIALEADFSDKHHLFLGRGD 475	C;Accession: AD3595	C;Accession: AD3595	C;Accession: AD3595
Db 419 AVTLAKVRLGLSVEDEARYTEERQLPSSQHQLNLEQIAQWAAQQAKFTQLFLRG1 478	Db 419 AVTLAKVRLGLSVEDEARYTEERQLPSSQHQLNLEQIAQWAAQQAKFTQLFLRG1 478	Db 419 AVTLAKVRLGLSVEDEARYTEERQLPSSQHQLNLEQIAQWAAQQAKFTQLFLRG1 478	Glutamine-fructose-6-phosphate transaminase (isomerizing)	Glutamine-fructose-6-phosphate transaminase (isomerizing)	Glutamine-fructose-6-phosphate transaminase (isomerizing)
Qy 476 QPIIALEGALKLKEIISYTHAAYAAGELKHPPLALIDADMPIVIVAPPNNEELFKLNSIE 535	Qy 476 QPIIALEGALKLKEIISYTHAAYAAGELKHPPLALIDADMPIVIVAPPNNEELFKLNSIE 535	Qy 476 QPIIALEGALKLKEIISYTHAAYAAGELKHPPLALIDADMPIVIVAPPNNEELFKLNSIE 535	C;Accession: AD3595	C;Accession: AD3595	C;Accession: AD3595
Db 479 HYPALEGALKLKEIITYTHAAXPAGEKHPPLALDVPVYAPNDSLIDKVKANMQ 538	Db 479 HYPALEGALKLKEIITYTHAAXPAGEKHPPLALDVPVYAPNDSLIDKVKANMQ 538	Db 479 HYPALEGALKLKEIITYTHAAXPAGEKHPPLALDVPVYAPNDSLIDKVKANMQ 538	Brucella melitensis	Brucella melitensis	Brucella melitensis
Qy 516 EVPARGGOLYVFAQDAGFVSSDMHTEMPKVEETIAPTFVTPQOLLAVHVALIKGT 594	Qy 516 EVPARGGOLYVFAQDAGFVSSDMHTEMPKVEETIAPTFVTPQOLLAVHVALIKGT 594	Qy 516 EVPARGGOLYVFAQDAGFVSSDMHTEMPKVEETIAPTFVTPQOLLAVHVALIKGT 594	R;Tetcelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Halt, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Puri, H.; Qin, H.; Vamathev, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizzi, A.;	R;Tetcelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Halt, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Puri, H.; Qin, H.; Vamathev, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizzi, A.;	R;Tetcelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Halt, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Puri, H.; Qin, H.; Vamathev, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizzi, A.;
Db 539 EVGARGGELFVFDLDSNFTNATSGVHTRAPRPHVGE-LSPVYHTIPVQOLLSTHVALARGT 597	Db 539 EVGARGGELFVFDLDSNFTNATSGVHTRAPRPHVGE-LSPVYHTIPVQOLLSTHVALARGT 597	Db 539 EVGARGGELFVFDLDSNFTNATSGVHTRAPRPHVGE-LSPVYHTIPVQOLLSTHVALARGT 597	Science 287, 1809-1815, 2000	Science 287, 1809-1815, 2000	Science 287, 1809-1815, 2000
Qy 595 DVQPRNLAKSVTVE 609	Qy 595 DVQPRNLAKSVTVE 609	Qy 595 DVQPRNLAKSVTVE 609	RESULTS 14	RESULTS 14	RESULTS 14
Db 598 DVQPRNLAKSVTVE 612	Db 598 DVQPRNLAKSVTVE 612	Db 598 DVQPRNLAKSVTVE 612	B81246	B81246	B81246
Qy 596 VDQPRNLAKSVTVE 609	Qy 596 VDQPRNLAKSVTVE 609	Qy 596 VDQPRNLAKSVTVE 609	RESULTS 15	RESULTS 15	RESULTS 15
Db 599 VDQPRNLAKSVTVE 612	Db 599 VDQPRNLAKSVTVE 612	Db 599 VDQPRNLAKSVTVE 612	RESULTS 15	RESULTS 15	RESULTS 15

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A; Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*
 A; Reference number: AD3222; PMID:1175688
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-612 <KUR>
 A; Cross-references: UNIPROT:QBYC47 ; UNIPARC:UPI000005859C ; GB:AE008918 ; PIDN:AAL53927.1;
 A; Experimental source: strain 16M
 A; Gene: BMEI0685
 A; Map position: II
 C; Superfamily: Glutamine-fructose-6-phosphate aminotransferase (isomerizing)
 C; Keywords: aminotransferase; isomerase

Query Match 47.0%; Score 1449; DB 2; Length 612;
 Best Local Similarity 49.3%; Pred. No. 9.6e-86;
 Matches 302; Conservative 99; Mismatches 202; Indels 10; Gaps 6;

Qy 1 MCGIVGAIQDVAELLEGLRLRRLYRGDSAGLAVDDEGHMTPLRRLGKVQMLAQAE 60
 Db 6 MCGIIIGIIGDEVAEVLVDAKLKRLEYRGDSAGATLQ-NGLRDRRAEGLVLEKRLA 64
 Qy 61 EHPLHGGTGAHTRWAHGEPSEVNAHPVSEHTVVVNGIENHEPLREELKARGTYFV 120
 Db 65 GEPLPGVIGIHTRWAHGEPVNAHPVTRALAVVHNGIENPAELAMLEAEGKTE 124
 Qy 121 SETDVEIAHLVNLWKLKGCGTIREAVLRAAPOLGAYGTIVMDSRHPTDILAAFSGSPVY 180
 Db 125 TETDTEAVALVTRLELEKGSKPVEAVRCDLPHLKGAFALAFPLGDEELLIGARQGPPLA 184
 Qy 181 IGLGMGENFIASDQLLPLPTTRRFIFLEEDIAETRSYNTIDFDTGAEVKRDIESNQ 240
 Db 185 VGYGEDEMFLGSDATAFLAPFTDTISLEDDWAVLTRNGSYIYDNNKKVVERPVQKSONT 244
 Qy 241 YDAGDKGTYIYHMQKEIYOPNAIKNTLGR --SHGQVDLSELGPNADELLSKVHEIQI 298
 Db 245 NMLVSKGNHRHFMQXEMFPEQEVISHTLANYLDFITGKVRKEAIGD---FSKVDRLTI 300
 Qy 299 LACGTSYNNSMVSRYWFEISLAGTIPCDVEASEFPRYKSAVRRNLSMITSQSQSGETADTA 358
 Db 301 TACGTPAYAATVAKWFEQIARLPVDSDASEFRYRMPLSKDSLAMFVQSQSGETADTA 360
 Qy 359 GLRISKELGWGLGSLAICNVPGSSLVRESIDALMTNAGTIGVASTKAKFTQLTIVLMLVA 418
 Db 361 SLRYCKAQQ-LKIASVLNTVGTSTIARESDAVFPTLAGEPVGSTAKFTQCLSMASLLA 419
 Qy 419 KLSRLKG-LDASIEHDIVRGLQALPSRIEQMLSDQKRIBALAEDFSKHALFLGRGDOY 477
 Db 420 AAARARGAIDEVREOBVLHOLSEAPRFINQVLEQDIAVCHDLSKVHVLVLRGTSF 479
 Qy 478 PIALEGALKLUKEISYTHAEGYAAEGFLKGKHPGLALIDAMPVIVVAPNNELLEKUKSNIEV 537
 Db 480 PLAMEGALKLUKEISYTHAEGYAAEGFLKGKHPGLKGKPIALIDETMVVITAPSDRYEVTVSNMQUEV 539
 Qy 538 RARGQOLYVFD-QDAGFVSSDNGHIIEMPHVEEVIAFPYTVPLQLLAYHVALIKGTDV 596
 Db 540 AARGRILLIITDKKGAEASISIDTMATIVLPEVPERISPLVYALPIQMAYHTAVLMLGTDV 599
 Qy 597 DQPRNLAKSVTVE 609
 Db 600 DQPRNLAKSVTVE 612

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 7, 2006, 09:21:51 ; Search time 153 Seconds
(without alignments)

3681.925 Million cell updates/sec
Title: US-10-612-779-2

Perfect score: 3086
Sequence: 1 MCIGVGAIAORDVAEILLEG.....LIKGTDVDQPRNLAKSVTVE 609

Scoring table: BL05UM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters:

2849598

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 7.2:
1: uniprot_sprot:
2: uniprot_trembl:
*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARES

Result No.	Score	Query	Match length	DB	ID	Description
1	3086	100.0	609	2	Q2MB847_ECOLI	Q2MB847 escherichia
2	3081	99.8	608	1	GLMS_ECOLI	P1769 e Glucosami
3	3081	99.8	609	2	Q32988_SHIDS	P3298 shigella dy
4	3079	99.8	609	2	Q31109_SHBRS	Q31109 shigella bo
5	3077	99.7	608	1	GLMS_ECOLI	Q8xe92 e glucosami
6	3077	99.7	608	1	GLMS_SHIFL	Q8iy4 e glucosami
7	3073	99.6	609	2	Q3YVN3_SHISS	Q3YVN3 shigella so
8	3067	99.4	608	1	GLMS_ECOLI	Q8fbt4 e glucosami
9	3058	99.1	608	1	GLMS_SALPA	Q5pv9 s glucosami
10	3058	99.1	609	2	Q57H72_SALCH	Q57H72 salmonella
11	3055	99.0	608	1	GLMS_SALTY	Q8zlx1 s glucosami
12	3049	98.8	608	1	GLMS_HAETN	Q8zq2 s glucosami
13	2681.5	86.9	609	1	GLMS_ERWC7	Q6cyj9 e glucosami
14	2677	86.7	608	1	GLMS_ERPE	Q8288 y glucosami
15	2677	86.7	608	1	GLMS_SALPA	Q6539r1 y glucosami
16	2555	83.1	608	1	GLMS_PHORR	Q7na97 p glucosami
17	2546.5	82.5	610	2	Q2NQ53_SOD1	Q2NQ53 sodalis g10
18	2274.5	73.7	610	2	Q4QNB6_HAET8	Q4qnb6 haemophilus
19	2265.5	73.4	609	1	GLMS_HAETN	P44708 h glucosami
20	2261.5	73.3	609	1	GLMS_VIBFL	Q5e279 v glucosami
21	2259.5	73.2	609	1	GLMS_VIBCH	Q9kum8 v glucosami
22	2245.5	72.8	609	1	GLMS_PHORR	Q61lh3 p glucosami
23	2230.5	72.3	609	1	GLMS_VIBPA	Q87r3 v glucosami
24	2224.5	72.1	609	1	GLMS_VIBVU	Q8gef3 v glucosami
25	2222.5	72.0	609	1	GLMS_VIBVY	Q7mp62 v glucosami
26	2212.5	71.7	610	2	Q3BG75_ACSC	Q3g9xs actinobacil
27	2197.5	71.2	609	1	GLMS_PASMU	P57963 p glucosami
28	2180.5	70.7	610	2	Q47UE2_COP3	Q47ue2 colwellia p
29	2159	70.0	609	2	Q33SL7_9GAMM	Q33sl7 shewanella p
30	2159	70.0	609	2	Q3P1V9_9GAMM	Q3p1v9 shewanella p
31	2156	69.9	609	2	Q3Q819_9GAMM	Q3q819 shewanella p

ALIGNMENTS

RESULT 1						
ID	Q2MB847_ECOLI	PRELIMINARY:	PRT:	609	AA:	
AC	Q2MB847;					
DT	21-FEB-2006,	Integrated into UniProtKB/TREMBL.				
DT	21-FEB-2006,	Sequence version 1.				
DT	07-MAR-2006,	Entry version 2.				
DE	L-Glutamine-D-fructose-6-phosphate aminotransferase.					
GN	Name=gimS;					
OS	Escherichia coli W3110					
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;					
OC	Enterobacteriaceae; Escherichia.					
NCBI_TaxID	316407;					
RN	[1]					
RP	NUCLEOTIDE SEQUENCE.					
RC	STRAIN=K-12;					
RC	SPRAINK-K-12;					
RA	Sekiuchi T., Ortega-Cesena J., Nosoh Y., Ohashi S., Tsuda K., Kanaya S.,					
RA	Smith D.R., Calvo J.M.;					
RT	"Nucleotide sequence of the E. coli gene coding for dihydrofolate reductase."					
RT	"Nucleotide sequence of the E. coli gene coding for dihydrofolate reductase."					
RL	Nucleic Acids Res. 8:2255-2274(1980).					
RN	[2]					
RP	NUCLEOTIDE SEQUENCE.					
RC	SPRAINK-K-12;					
RC	Strain=K-12;					
RA	Chen H., Sun Y., Stark T., Beattie W., Moses R.E.;					
RA	"Nucleotide sequence and deletion analysis of the polB gene of Escherichia coli."					
RT	"Nucleotide sequence and deletion analysis of the polB gene of Escherichia coli."					
RT	Escherichia coli K-12.					
RT	Genetics (Life Sci. Adv.) 11:59-65 (1992).					
RL	DNA Cell Biol. 9:613-635 (1990).					
RN	[3]					
RP	NUCLEOTIDE SEQUENCE.					
RC	STRAIN=K-12;					
RC	Smallshaw J.E., Kelln R.A.;					
RA	Hayashi K., Morooka N., Yamamoto Y., Fujita K., Isono K., Choi S., Onitsubo E., Baba T., Wanner B.L., Mori H., Horiuchi T.;					
RT	"Cloning, nucleotide sequence and expression of the polB gene of Escherichia coli."					
RT	"Nucleotide sequence and deletion analysis of the polB gene of Escherichia coli."					
RT	Escherichia coli K-12.					
RT	Genetics (Life Sci. Adv.) 11:59-65 (1992).					
RL	DNA Cell Biol. 9:613-635 (1990).					
RN	[4]					
RP	NUCLEOTIDE SEQUENCE.					
RC	STRAIN=K-12;					
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RT	"Cloning, nucleotide sequence and expression of the polB gene of Escherichia coli."					
RT	"Nucleotide sequence and deletion analysis of the polB gene of Escherichia coli."					
RT	Escherichia coli K-12.					
RT	Genetics (Life Sci. Adv.) 11:59-65 (1992).					
RL	DNA Cell Biol. 9:613-635 (1990).					
RN	[5]					
RP	NUCLEOTIDE SEQUENCE.					
RC	STRAIN=K-12;					
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RA	Hayashi K., Morooka N., Yamamoto Y., Fujita K., Isono K., Choi S., Onitsubo E., Baba T., Wanner B.L., Mori H., Horiuchi T.;					
RT	"Cloning, nucleotide sequence and expression of the polB gene of Escherichia coli."					
RT	"Nucleotide sequence and deletion analysis of the polB gene of Escherichia coli."					
RT	Escherichia coli K-12.					
RT	Genetics (Life Sci. Adv.) 11:59-65 (1992).					
RL	DNA Cell Biol. 9:613-635 (1990).					
RN	[6]					
RP	NUCLEOTIDE SEQUENCE.					

RC STRAIN=K-12; PubMed=16397293; DOI=10.1093/nar/gkj150;
 RA Riley M., Abe T., Arnaud M.B., Berlyn M.K., Blattner F.R.,
 RA Chaudhuri R.R., Glesner J.D., Horiuchi T., Kessler I.M., Kosuge T.,
 RA Mori H., Perna N.T., Rudd G. III., Thomas G.H., Thomson N.R.,
 RA "Escherichia coli K-12: a cooperatively developed annotation snapshot-
 RT -2005.",
 RL Nucleic Acids Res. 34:1-9 (2006).
 RN [7]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K-12;
 RX MEDLINE=97349980; PubMed=9205837; DOI=10.1093/dnarecs/4.2.9.1;
 RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
 RA Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nishimoto H.,
 RA Oyama S., Saito N., Sanpei G., Satoh Y., Sivasundaram S.,
 RA Tashiro H., Takahashi H., Takeda J., Takedo K., Uehara K., Wada C.,
 RA Yamagata S., Horiuchi T.;
 RT "Construction of a contiguous 874-kb sequence of the Escherichia coli
 -K12 genome corresponding to 50.0-68.8 min on the linkage map and
 RT analysis of its sequence features.",
 RN DNA Res. 4:91-113 (1997).
 RN [8]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K-12;
 RX MEDLINE=97251358; PubMed=9097040; DOI=10.1093/dnarecs/3.6.379;
 RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
 RA Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
 RA Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S.,
 RA Nishimoto H., Nisio Y., Oshima T., Saito N., Sampei G., Seki Y.,
 RA Sivasundaram S., Tagami H., Takeda J., Takedo K., Wada C.,
 RA Yamamoto Y., Horiuchi T.;
 RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
 RT corresponding to the 40.1-50.0 min region on the linkage map.",
 RL DNA Res. 3:379-392 (1996).
 RN [9]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K-12;
 RX MEDLINE=97251357; PubMed=9097039; DOI=10.1093/dnarecs/3.6.363;
 RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
 RA Kasai H., Nishimoto K., Kimura S., Kitakawa M., Kitagawa M.,
 RA Makino K., Miki T., Mizobuchi K., Mori H., Motomura K.,
 RA Nakade S., Nakamura Y., Nishimoto H., Mori T., Nishio Y.,
 RA Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J.,
 RA Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
 RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
 RT corresponding to the 28.0-40.1 min region on the linkage map.",
 RL DNA Res. 3:363-377 (1996).
 RN [10]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K-12;
 RX MEDLINE=97094878; PubMed=8940112; DOI=10.1074/jbc.271.49.31145;
 RA Arn E.A., Abelson J.N.;
 RT "The 2'-5' RNA ligase of Escherichia coli. Purification, cloning, and
 RT genomic disruption.",
 RL J. Biol. Chem. 271:31145-31153 (1996).
 RN [11]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K-12;
 RX MEDLINE=97061202; PubMed=8905232; DOI=10.1093/dnarecs/3.3.137;
 RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
 RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanaai K., Kashimoto K.,
 RA Kimura S., Kitagawa M., Makino K., Nishimoto H., Nishio Y., Saito N.,
 RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
 RA Sampei G., Seki Y., Tagami H., Takedo K., Wada C., Yamamoto Y.,
 RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
 RT corresponding to the 12.7-28.0 min region on the linkage map.",
 RL DNA Res. 3:137-155 (1996).
 RN [12]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K-12;

RX MEDLINE=94261430; PubMed=8202364;
 RA Fujita N., Mori H., Yura T., Ishihama A.;
 RT "Systematic sequencing of the Escherichia coli genome: analysis of the
 RT 2.4-4.1 min (110,917-193,643 bp) region.",
 RL Nucleic Acids Res. 22:1637-1639 (1994).
 RN [13]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K-12;
 RX MEDLINE=94240115; PubMed=8183997;
 RA Janos L., Shimizu I., Kaji A.;
 RT "Ribosome recycling factor (ribosome releasing factor) is essential
 RT for bacterial growth.",
 RL Proc. Natl. Acad. Sci. U.S.A. 91:4249-4253 (1994).
 RN [14]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K-12;
 RX MEDLINE=94124004; PubMed=7904973; DOI=10.1016/0378-1119(93)90470-N;
 RA Allikmets R., Gerrard B.C., Court D., Dean M.C.;
 RT "Cloning and organization of the abc and mdl genes of Escherichia
 coli: relationship to eukaryotic multidrug resistance.",
 RL Gene 136:231-236 (1993).
 RN [15]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K-12;
 RX MEDLINE=9418640; PubMed=8412694;
 RA van Heeswijk W.C., Rabenhorst M., Westerhoff H.V., Kahn D.D.;
 RT "The genes of the glutamine synthetase adenyllylation cascade are not
 RT regulated by nitrogen in Escherichia coli.",
 RL Mol. Microbiol. 9:443-458 (1993).
 RN [16]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K-12;
 RX MEDLINE=9259920; PubMed=8387990;
 RA Zhao S., Sandt C.H., Feulner G., Vlazny D.A., Hill C.W.;
 RT "Rhs elements of Escherichia coli K-12: complex composites of shared
 RT and unique components that have different evolutionary histories.",
 RL J. Bacteriol. 175:2799-2808 (1993).
 RN [17]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K-12;
 RX MEDLINE=91231180; PubMed=8419307;
 RA Yamada M., Asaka S., Saier M.H. Jr., Yamada Y.;
 RT "Characterization of the gcd gene from Escherichia coli K-12 W3110 and
 RT regulation of its expression.",
 RL J. Bacteriol. 175:568-571 (1993).
 RN [18]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K-12;
 RX MEDLINE=93116053; PubMed=1474579;
 RA Cormack R.S., Mackie G.A.;
 RT "Structural requirements for the processing of Escherichia coli 5 S
 RT ribosomal RNA by RNase E in vitro.",
 RL J. Mol. Biol. 228:1078-1090 (1992).
 RN [19]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K-12;
 RX MEDLINE=93094132; PubMed=1459951;
 RA Gervais F.G., Drapeau G.R.;
 RT "Identification, cloning, and characterization of rcsF, a new
 RT regulator gene for exopolysaccharide synthesis that suppresses the
 RT division mutation ftsZ84 in Escherichia coli K-12.",
 RL J. Bacteriol. 174:8016-8022 (1992).
 RN [20]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K-12;
 RX MEDLINE=93077430; PubMed=1447125;
 RA Yamamoto K., Ogura T., Niki H., Hiraga S.;
 RT "Identification and characterization of the smba gene, a suppressor of
 RT the mukB null mutant of Escherichia coli.",
 RL J. Bacteriol. 174:7517-7526 (1992).
 RN [21]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K-12;

RX	MEDLINE=93011013; PubMed=1396599;	the sequence of a 17 kilobase segment containing <i>asnA</i> , <i>oriC</i> , <i>unc</i> , <i>91ms</i> and <i>phos</i> .";
RA	Condon C., Phillips J., Fu Z.Y., Squires C., Squires C.L.;	Biochem. J. 224:799-815(1984).
Query Match	100.0% Score: 3086; DB: 2; Length: 609;	
Best Local Similarity	100.0% Pred. No. 2.8e-186;	
Matches	609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Db	1 MCGIVGAIORDVAILLGLRRLREYRGDSAGLAVIDAEGMTLRLRIGKVQMLAQAE 60	RT NUCLEOTIDE SEQUENCE [GENOMIC DNA].
Db	1 MCGIVGAIORDVAILLGLRRLREYRGDSAGLAVIDAEGMTLRLRIGKVQMLAQAE 60	RT NUCLEOTIDE SEQUENCE [GENOMIC DNA].
Qy	61 EPHLHGTTGTAHTRWATGEPSYESEHIVVANGIENHEPLREELKARGTTFV 120	RT NUCLEOTIDE SEQUENCE [GENOMIC DNA].
Db	61 EPHLHGTTGTAHTRWATGEPSYESEHIVVANGIENHEPLREELKARGTTFV 120	RT NUCLEOTIDE SEQUENCE [GENOMIC DNA].
Qy	121 SETDTEVIAHLVNLKQGTLRPAVLRAIPQURGAYGTIVIMSRHPTDILAAARGSPV 180	RT NUCLEOTIDE SEQUENCE [GENOMIC DNA].
Db	121 SETDTEVIAHLVNLKQGTLRPAVLRAIPQURGAYGTIVIMSRHPTDILAAARGSPV 180	RT NUCLEOTIDE SEQUENCE [GENOMIC DNA].
Qy	181 IGLGMGENFTASDQLLIVTRRFLEQDIAIRTRRSVNIFDKTAGVKEVKRDIESNLQ 240	RT NUCLEOTIDE SEQUENCE [GENOMIC DNA].
Db	181 IGLGMGENFTASDQLLIVTRRFLEQDIAIRTRRSVNIFDKTAGVKEVKRDIESNLQ 240	RT NUCLEOTIDE SEQUENCE [GENOMIC DNA].
Qy	241 YDAGDKGTRHYMOKETIYQPNIAKNTLTGRISHQVDLSELGPNADELSSKVHEIQIQLA 300	RT NUCLEOTIDE SEQUENCE [GENOMIC DNA].
Db	241 YDAGDKGTRHYMOKETIYQPNIAKNTLTGRISHQVDLSELGPNADELSSKVHEIQIQLA 300	RT NUCLEOTIDE SEQUENCE [GENOMIC DNA].
Qy	301 CGTSYNSGIVSRYMFEISLGIQPCDVEIASEFRYKSAVRSNIMITLSQSGETADTLAGL 360	RT NUCLEOTIDE SEQUENCE [GENOMIC DNA].
Db	301 CGTSYNSGIVSRYMFEISLGIQPCDVEIASEFRYKSAVRSNIMITLSQSGETADTLAGL 360	RT NUCLEOTIDE SEQUENCE [GENOMIC DNA].
Qy	361 RLSKELGIGVGLSLACNVPSQSLIRESDLMITNGATEGVASTKAFTQTLVILMLVAKL 420	RT NUCLEOTIDE SEQUENCE [GENOMIC DNA].
Db	361 RLSKELGIGVGLSLACNVPSQSLIRESDLMITNGATEGVASTKAFTQTLVILMLVAKL 420	RT NUCLEOTIDE SEQUENCE [GENOMIC DNA].
Qy	422 SRLKGLDASIEHDIVHGLALPSRSEIQLMFEISLGIQPCDVEIASEFRYKSAVRSNIMITLSQSGETADTLAGL 360	RT NUCLEOTIDE SEQUENCE [GENOMIC DNA].
Db	422 SRLKGLDASIEHDIVHGLALPSRSEIQLMFEISLGIQPCDVEIASEFRYKSAVRSNIMITLSQSGETADTLAGL 360	RT NUCLEOTIDE SEQUENCE [GENOMIC DNA].
Qy	481 LEGALKLKRISYTHAEA7AAGELKKGPLALIDAMPVIVAPNNELEKLSKNEEYRAR 540	RT CHARACTERIZATION.
Db	481 LEGALKLKRISYTHAEA7AAGELKKGPLALIDAMPVIVAPNNELEKLSKNEEYRAR 540	RT MEDLINE=88281539; PubMed=3134953; DOI=10.1016/0300-9084(88)90073-9;
Qy	541 GGQLYVFAQDAGTVSSDMH1IEMPAYEVIAPIFYTVPLQLLAYHALIKSTDVQPR 600	RT Dutka-Malen S., Mazodier P., Badet B.;
Db	541 GGQLYVFAQDAGTVSSDMH1IEMPAYEVIAPIFYTVPLQLLAYHALIKSTDVQPR 600	RT Polikarpov I., Littlechild J.A., Teplyakov A.;
Qy	601 NLAKSVTVE 609	RT "Sequence requirements of the glucosamine synthetase gene from <i>Escherichia coli</i> .";
Db	601 NLAKSVTVE 609	RT "Substrate binding is required for assembly of the active conformation of the catalytic site in Ncm amidotransfases: evidence from the 1.8-A crystal structure of the Glutaminase domain of glucosamine 6-phosphate synthase";
RESULT 2		RT "Involvement of the C terminus in intramolecular nitrogen channeling in glucosamine 6-phosphate synthase: evidence from a 1.6-A crystal structure 6:104-7-1055(1998)."
GLMS_ECOLI	STANDARD; PRT; 608 AA.	RT X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 241-608.
ID	GIMs_ECOLI STANDARD; PRT; 608 AA.	RT MEDLINE=9614326; PubMed=8605567; DOI=10.1016/S0969-2126(96)00087-1;
AC	P17169; P76745; 01-AUG-1990, integrated into UniProtKB/Swiss-Prot.	RT Isupov M.N., Obmolova G., Butterworth S., Badet-Denisot M.-A., Badet B.;
DT	15-DEC-1998, sequence version 3.	RT Polikarpov I.;
DE	07-MAR-2005, entry version 70.	RT "Involvement of the C terminus in intramolecular nitrogen channeling in glucosamine 6-phosphate synthase: evidence from a 1.6-A crystal structure 6:104-7-1055(1998)."
DE	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] (EC 2.6.1.16) (Hexosephosphate aminotransferase) (D-fructose-6-phosphate amidotransferase) (GPAT) (L-glutamin-D-fructose-6-phosphate amidotransferase) (Glucosamine-6-phosphate synthase).	RT X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 241-608.
DE	Name=gimS; OrderdLocusName=b3729; Escherichia coli.	RT MEDLINE=99190083; PubMed=10091662;
OS	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.	RT "The mechanism of sugar phosphate isomerization by glucosamine 6-phosphate synthase.";
OC		RT Protein Sci. 8:546-605(1999).
NCBI_TaxID	562;	RT "- FUNCTION: Catalyzes the first step in hexosamine metabolism,
RN		"DNA sequence around the <i>Escherichia coli</i> unc operon. Completion of
RP	NUCLEOTIDE SEQUENCE [GENOMIC DNA].	
RX	MEDLINE=85121806; PubMed=6398585;	
RA	Walker J.E., Gay N.J., Saraste M., Eberle A.N.;	
RT	"DNA sequence around the <i>Escherichia coli</i> unc operon. Completion of	

converting Fructose-6P into glucosamine-6P using glutamine as a nitrogen source.	FT	STRAND	8	8
CC	FT	TURN	91	92
CC	FT	STRAND	93	101
CC	FT	TURN	102	103
CC	FT	HELIX	104	113
- I- SUBUNIT: Homodimer.	FT	TURN	114	115
- I- INTERACTION: P09571.alas; NbExp=1; IntAct=EBI-551022, EBI-544061;	FT	STRAND	120	120
CC	FT	STRAND	123	123
CC	FT	HELIX	124	136
P76552; eutH; NbExp=1; IntAct=EBI-551022, EBI-551031;	FT	TURN	137	137
CC	FT	STRAND	138	139
P62615;1spB; NbExp=1; IntAct=EBI-551022, EBI-562203;	FT	STRAND	141	151
CC	FT	HELIX	154	162
P11751;rp1V; NbExp=1; IntAct=EBI-551022, EBI-551022;	FT	TURN	163	164
CC	FT	STRAND	166	167
P21166;trkH; NbExp=1; IntAct=EBI-551022, EBI-550288;	FT	STRAND	169	176
CC	FT	STRAND	179	182
P76093;ynbd; NbExp=1; IntAct=EBI-551022, EBI-551038;	FT	STRAND	184	185
CC	FT	STRAND	187	192
P33366;YohD; NbExp=1; IntAct=EBI-551022, EBI-551046;	FT	HELIX	193	195
CC	FT	TURN	196	199
- I- SUBCELLULAR LOCATION: Cyttoplasm.	FT	STRAND	201	205
- I- SIMILARITY: In the C-terminal section; belongs to the SIS family.	FT	TURN	208	209
CC	FT	STRAND	211	214
CC	FT	STRAND	216	217
CC	FT	STRAND	219	222
CC	FT	TURN	224	225
CC	FT	STRAND	228	229
CC	FT	STRAND	233	235
CC	FT	TURN	246	247
CC	FT	STRAND	249	250
CC	FT	HELIX	251	257
CC	FT	TURN	258	258
CC	FT	HELIX	259	267
CC	FT	TURN	268	269
Query Match 99.8%; Score 3081; DB 1; Length 608;				
Best Local Similarity 100.0%; Pred. No. 5.8e-186;				
Matches 608; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	2	CGIVGATAQRDVAEILLEGRLRLEYRGYDSAGLAVDAGHMTTRRLGKYMQLAQAAE	61	
DR	1	CGIVGATAQRDVAEILLEGRLRLEYRGYDSAGLAVDAGHMTTRRLGKYMQLAQAAE	60	
DR	2	HPLHGGTCAIAHTRWATGEPESEVNAHPVSEHIVVNGIIEHPEPLREELKARGTIVVS	121	
DR	62	HPLHGGTCAIAHTRWATGEPESEVNAHPVSEHIVVNGIIEHPEPLREELKARGTIVVS	121	
DR	61	HPLHGGTCAIAHTRWATGEPESEVNAHPVSEHIVVNGIIEHPEPLREELKARGTIVVS	120	
DR	122	ETDTEVIAHNLWELKQGTLREAVLAIQPLRGAYTGVIMDSRHPDTLLAARSGLPVLVI	181	
DR	121	ETDTEVIAHNLWELKQGTLREAVLAIQPLRGAYTGVIMDSRHPDTLLAARSGLPVLVI	180	
DR	182	GI/GMGENTIASDOLALLPVTTRFLFEGDIAETRRSVNLPDKTGAAEVKRDIESNLQY	241	
DR	181	GLGNGENTIASDOLALLPVTTRFLFEGDIAETRRSVNLPDKTGAAEVKRDIESNLQY	240	
DR	242	DAGDKGIVYRHYMKKEYQPNIAKNTLTGRISHGQDLSLGPNADLSKVEHIIQILAC	301	
DR	241	DAGDKGIVYRHYMKKEYQPNIAKNTLTGRISHGQDLSLGPNADLSKVEHIIQILAC	300	
DR	302	GTSYNSGMVSRYWFEFLAGIPCDVEIAFVRKSAVVRNSLMTLSQGETADTLGLR	361	
DR	361	LSKELGYLGSLAICNPGSSLYRESLALMTNAGTEIVGAVSTAKFTQTLVLLMLYAKLS	421	
DR	422	DAGDKGIVYRHYMKKEYQPNIAKNTLTGRISHGQDLSLGPNADLSKVEHIIQILAC	301	
DR	421	RKGGLDASIEHDIVHGLQALPSRQEQLSODKRIEALAEFSDKHAFLFLGRGQDQYIAL	481	
DR	85	EGALKLKEISYIHAAYAAGELKHGHPIALIDADMPPNELLKSNTEEVARG	541	
QY	1	181		
REGION	1	1		
ACT SITE	1	1		
ACT SITE	603	603		
CONFICT	418	419		
FT	2	7		
STRAND	9	10		
STRAND	13	26		
STRAND	29	36		
STRAND	38	39		
STRAND	42	49		
STRAND	51	60		
STRAND	61	61		
STRAND	66	73		
STRAND	76	78		
STRAND	80	81		
TURN	82	84		
STRAND	85	86		

Db	481	EGALKLKEISVIIAAYAAGELKRGPLALLADMPVIVAPPNELLEKLKSNIEEVARG	540	Qy	301	CGTTSYNSGMVSRWPEFESLAGIPCDVETIASEFPRYKSAVRNSLMTLSQSGETADTLAGL	360			
Qy	542	GOLYYFADQDGFFVSSDNMHIEMPHVEETAPIFYTVPLQLLAYHVALKGTDVQPRN	601	Db	301	CGTTSYNSGMVSRWPEFESLAGIPCDVETIASEFPRYKSAVRNSLMTLSQSGETADTLAGL	360			
Db	541	GOLYYFADQDGFFVSSDNMHIEMPHVEETAPIFYTVPLQLLAYHVALKGTDVQPRN	600	Qy	361	RLSKELGTLGSLAIQNPQSSLVRESDLALMTNAGEIGVASTKRAFTQTLVLLMVLVAKL	420			
Qy	602	LAKSVTVE	609	Db	361	RLSKELGTLGSLAIQNPQSSLVRESDLALMTNAGEIGVASTKRAFTQTLVLLMVLVAKL	420			
Db	601	LAKSVTVE	608	Qy	421	SRLKGLDASIEHDIVGLQALPSEEQMLSQDKRIBALADFSQDGHALFGRGDQYPIA	480			
RESULT 3										
	Q329R8_SHIDS	SHIDS	PRELIMINARY;	PRT;	609	AA.				
ID	Q329R8_-	SHIDS								
AC	Q329R8_-	SHIDS								
DT	06-DEC-2005	integrated into UniProtKB/TREMBL.								
DT	06-DEC-2005	sequence version 1.								
DT	07-FEB-2006	entry version 4.								
DE	L-glutamine:D-fructose-6-phosphate aminotransferase.									
GN	Name=GlnS; OrderedLocusName=SDY 4019;									
OS	Shigella dysenteriae serotype 1 (Strain Sd197).									
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;									
OC	Enterobacteriaceae; Shigella.									
OX	NCBI_TaxID=300267;									
RN	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].									
RX	PubMed=16275186; DOI=10.1093/nar/gki954;									
RA	Yang F., Yang J., Chen L., Xue Y., Yan Y., Tang X.,									
RA	Wang J., Xiong Z., Dong J., Xue Y., Yan Y., Tang X.,									
RA	Nie H., Peng J., Xu J., Wang Y., Yuan Z., Wen Y.,									
RA	Qiang B., Hou Y., Yu J., Jin Q.,									
RT	"Genome dynamics and diversity of <i>Shigella</i> species, the etiologic									
RT	agents of bacillary dysentery";									
RL	Nucleic Acids Res. 33:6445-6458 (2005).									
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms distributed under the Creative Commons Attribution-NoDerivs License									
CC	-----									
DR	EMBL; CP000034; AB663937.1; -; Genomic_DNA.									
DR	GO; GO:0005737; Cytoplasm; IEA.									
DR	GO; GO:004360; F-galutarane-fructose-6-phosphate transaminase. . . ; IEA.									
DR	GO; GO:005523; F:sugar binding; IEA.									
DR	GO; GO:016740; F:transferase activity; IEA.									
DR	GO; GO:0116051; F:carbohydrate biosynthesis; IEA.									
DR	GO; GO:005975; F:carbohydrate metabolism; IEA.									
DR	GO; GO:008152; F:metabolism; IEA.									
KW	Aminotransferase; Complete proteome; Transferase									
SQ	SEQUENCE 609 AA; 66994 MW; 637301513227484 CRC64;									
Query Match 99.8%; Score 3081; DB 2; Length 609;										
Best Local Similarity 99.8%; Pred. No. 5.8e-186;										
Matches 608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;										
Qy	1 MCGIVGAIQRDVAELLGSLRRLYRGYASGLAVDQHGMTRLLRGVQMLAQAA	60	CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms distributed under the Creative Commons Attribution-NoDerivs License						
Db	1 MCGIVGAIQRDVAELLGSLRRLYRGYASGLAVDQHGMTRLLRGVQMLAQAA	60	CC	-----						
Qy	61 EHPLGGTGTAAHTRWAHGPESEVNAHYPHSEHIVVNGTENHEPLRPLKARGYTFV	120	DR	EMBL; CP000336; ABB68229.1; -; Genomic_DNA.						
Db	61 EHPLGGTGTAAHTRWAHGPESEVNAHYPHSEHIVVNGTENHEPLRPLKARGYTFV	120	DR	GO; GO:0005737; C:cytoplasm; IEA.						
Qy	121 SETDTEVIAHLVNLKOGGTIREAVTRAPOLRGAYGTIVMDSRHPDTLAAARSQSPV	180	DR	GO; GO:0004360; F:glutaminato-fructose-6-phosphate transaminase. . . ; IEA.						
Db	121 SETDTEVIAHLVNLKOGGTIREAVTRAPOLRGAYGTIVMDSRHPDTLAAARSQSPV	180	DR	GO; GO:0005229; F:sugar binding; IEA.						
Qy	181 IGLGNGENFASDQLALLPTRRFLPSEGDAIETRRSNIFDKTGAEVRQDIESNLQ	240	DR	GO; GO:016740; F:transferase activity; IEA.						
Db	181 IGLGNGENFASDQLALLPTRRFLPSEGDAIETRRSNIFDKTGAEVRQDIESNLQ	240	DR	GO; GO:0016051; F:carbohydrate biosynthesis; IEA.						
Qy	241 YDAGDKGIVYHYMOKEIYEOPNAIKNTLGRISHGQYDLSLGPNADELLSKVHEIQI	300	DR	GO; GO:0005975; F:metabolism; IEA.						
Db	241 YDAGDKGIVYHYMOKEIYEOPNAIKNTLGRISHGQYDLSLGPNADELLSKVHEIQI	300	DR	GO; GO:0008152; P:transferase; IEA.						
Qy	61 EHPLGGTGTAAHTRWAHGPESEVNAHYPHSEHIVVNGTENHEPLRPLKARGYTFV	120	DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.						

Db	61. EHPHGTTAHTWATCCEPSBAAHPPVSEHIMVNGILENHEPREELKARGTFFV 120	RA	Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasaki C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H., "Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12." ; RT DNA Res. 8:11-22 (2001).
Qy	121. SETDTEVIAHLVNLKQGTLPRAVLRAIPOQRGATGTVIMPSRHPDPTLAAARGSPLV 180	RA	"-";
Db	121. SETDTEVIAHLVNLKQGTLPRAVLRAIPOQRGATGTVIMPSRHPDPTLAAARGSPLV 180	RT	"-";
Qy	181. IGLGMGENFTASDOLALLPVTTRFIFLEGGDIAETRVSFNFDKTAEVKRDIESNLQ 240	CC	"-";
Db	181. IGLGMGENFTASDOLALLPVTTRFIFLEGGDIAETRVSFNFDKTAEVKRDIESNLQ 240	CC	"-";
Qy	241. YDAGDKGIYRHQKEIYEQPNAIKNTLTGRISHQVDSELGPNADELSSKVEH1QIQA 300	CC	"-";
Db	241. YDAGDKGIYRHQKEIYEQPNAIKNTLTGRISHQVDSELGPNADELSSKVEH1QIQA 300	CC	"-";
Qy	301. CGTISYNSGMVSRVYFESLQIPCDVETAEFVRKSAVRNSLMTISQSGETADTLAQL 360	CC	"-";
Db	301. CGTISYNSGMVSRVYFESLQIPCDVETAEFVRKSAVRNSLMTISQSGETADTLAQL 360	CC	"-";
Qy	361. RLSEKLGVLGSLATCNPGSSLYRESDLALMTNAGTEGVASTKAFTTQLTVLMLVAKL 420	CC	"-";
Db	361. RLSEKLGVLGSLATCNPGSSLYRESDLALMTNAGTEGVASTKAFTTQLTVLMLVAKL 420	CC	"-";
Qy	421. SRLKGLDASIEHDIVHGLQALPSRQEQLSDQKRIEALAEFSDKHALFLGRDQYPIA 480	CC	"-";
Db	421. SRLKGLDASIEHDIVHGLQALPSRQEQLSDQKRIEALAEFSDKHALFLGRDQYPIA 480	CC	"-";
Qy	481. LEGALKLKEISYIHAEAAYAGELKGPLALIDAMPVIVAPNNELEKLSNIEEVVAR 540	CC	"-";
Db	481. LEGALKLKEISYIHAEAAYAGELKGPLALIDAMPVIVAPNNELEKLSNIEEVVAR 540	CC	"-";
Qy	541. GGQLYVFAQDQAGFVSSDNMHI1EMPHVEVIAPIFYVPLQLLATHVALIKGTDVQPR 600	CC	"-";
Db	541. GGQLYVFAQDQAGFVSSDNMHI1EMPHVEVIAPIFYVPLQLLATHVALIKGTDVQPR 600	CC	"-";
Qy	601. NLAKSVTVE 609	CC	"-";
Db	601. NLAKSVTVE 609	CC	"-";
Qy	2 CGIVGAIAQDVAEILLEGLRRLERYGDSAGLAVDABGHMTRLRLGRVQMLAQAAEE 61	CC	"-";
Db	1 CGIVGAIAQDVAEILLEGLRRLERYGDSAGLAVDABGHMTRLRLGRVQMLAQAAEE 60	CC	"-";
RESULT 5			
GLMS_ECO57	STANDARD;	PRT;	608 AA.
ID	GLMS_ECO57	STANDARD;	PRT;
AC	QBXEG2;		
DT	11-JUL-2002, integrated into UniProtKB/Swiss-Prot.		
DT	11-JUL-2002, sequence version 2.		
DT	07-MAR-2006, entry version 24.		
DE	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]		
DE	(EC 2.6.1.16) (Hexosephosphate aminotransferase) (D-fructose-6-phosphate aminotransferase) (GFrAT) (L-glutamate-D-fructose-6-phosphate aminotransferase) (Glucosamine-6-phosphate synthase).		
DE	amidotransferase; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.		
GN	Name=gLms; OrderedLocusName=z3227; Ecs4671;		
OS	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.		
NCBI_TaxID	83334;		
RN	[1] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].		
RP	STRAIN=O157:H7 / EDL93 / ATCC2504089; MEDLINE=21074935; Published=1120651; DOI=10.1038/35054089; Perna N.T., Plunkett G. III., Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamitis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R., "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7." ; Nature 409:529-533 (2001).	Qy	62. HPLHGTGIAHTRWAHTGGESEVNAHPPHSEHIVVNGTENIHEPREELKARYTFFV 121
RP	STRAIN=O157:H7 / EDL93 / ATCC2504089; MEDLINE=21074935; Published=1120651; DOI=10.1038/35054089; Perna N.T., Plunkett G. III., Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamitis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R., "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7." ; Nature 409:529-533 (2001).	Db	61. HPLHGTGIAHTRWAHTGGESEVNAHPPHSEHIVVNGTENIHEPREELKARYTFFV 120
RP	STRAIN=O157:H7 / Sakai / RIM 050932 / EHEC; MEDLINE=21156231; Published=11258796; DOI=10.1093/dnare/8.1.11; Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Tokoyama K.,	Qy	122. ETDTETVIAHLVNLKQGTLPREAVRAIFQLRGAYGTIMDSRHPDTLAAARGSSPLVI 181
RP	STRAIN=O157:H7 / Sakai / RIM 050932 / EHEC; MEDLINE=21156231; Published=11258796; DOI=10.1093/dnare/8.1.11; Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Tokoyama K.,	Db	121. ETDTETVIAHLVNLKQGTLPREAVRAIFQLRGAYGTIMDSRHPDTLAAARGSSPLVI 180
RP	STRAIN=O157:H7 / Sakai / RIM 050932 / EHEC; MEDLINE=21156231; Published=11258796; DOI=10.1093/dnare/8.1.11; Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Tokoyama K.,	Qy	182. GLGMGENFTASDQALLPVTRFLFLEEGDIAETRVSFNFDKTAEVKRDIESNLQY 241
RP	STRAIN=O157:H7 / Sakai / RIM 050932 / EHEC; MEDLINE=21156231; Published=11258796; DOI=10.1093/dnare/8.1.11; Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Tokoyama K.,	Db	181. GLGMGENFTASDQALLPVTRFLFLEEGDIAETRVSFNFDKTAEVKRDIESNLQY 240

Qy	302	GTSNSGMVSYWFSLAGPCDVEIASPYRKSAVRSLMITSQSGETADTLAIGR	361	-- SIMILARITY: Contains 1 type-2 glutamine amidotransferase domain.
Db	301	GTSNSGMVSYWFSLAGPCDVEIASPYRKSAVRSLMITSQSGETADTLAIGR	360	--
Qy	362	LSKELGYLGSLLAICNPGSSILVRESDLALMTNAGTEIGVASTAKFTTQLTVLLVAKLS	421	--
Db	361	LSKELGYLGSLLAICNPGSSILVRESDLALMTNAGTEIGVASTAKFTTQLTVLLVAKLS	420	--
Qy	422	RLKGKDASIEFDIVHGLQALPSRTEQMLSDQKRIBALAEFSDKHFAFLGRGDQYPIAL	481	--
Db	421	RLKGKDASIEFDIVHGLQALPSRTEQMLSDQKRIBALAEFSDKHFAFLGRGDQYPIAL	480	--
Qy	482	EGALKLKEIISYHAYAAGELKGICPLALDADMPVTVAPPNELLKEKLSNIEEVTRARG	541	--
Db	481	EGALKLKEIISYHAYAAGELKGICPLALDADMPVTVAPPNELLKEKLSNIEEVTRARG	540	--
Qy	542	GOLYVFAODAGFVSSDNMHIEMPHVEETAPIFYTVPLQLLAYVALKGTDVDQPRN	601	--
Db	541	GOLYVFAEQAQGFVSSDNMHIEMPHVEETAPIFYTVPLQLLAYVALKGTDVDQPRN	600	--
Qy	602	LAKSVTVE	609	KW Aminotransferase; Complete proteome; Glutamine amidotransferase; KW Transferase.
Db	601	LAKSVTVE	608	KW
RESULT 6				
ID GLMS_SHIFL, STANDARD; PRT: 608 AA.				
AC Q831Y4; Q7BZ99; DT 30-AUG-2005; integrated into UniProtKB/Swiss-Prot.				
DT 07-MAR-2006; entry version 22.				
DE Glucosamine-f-fructose-6-phosphate aminotransferase [isomerizing] (EC 2.6.1.16) (Rexosephosphate aminotransferase) (D-fructose-6-phosphate amidotransferase) (GFAT) (L-glutamine-D-fructose-6-phosphate amidotransferase) (Glucosamine-6-phosphate synthase).				
Name=gims; OrderedDocusName=SF3899; S3959; Shigella flexneri.				
OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Shigella.				
OC NCBI_TaxID=623; RN				
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].				
RC SPRAIN-301 / Serotype 2a; MEDLINE=2227406; PubMed=12384590; DOI=10.1093/nar/gkf566; Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H., Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J., Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S., Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y., Yu J.; "Genome sequence of <i>Shigella flexneri</i> 2a: insights into pathogenicity through comparison with genomes of <i>Escherichia coli</i> K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).				
RN SPRAIN-2457T / ATCC 700930 / Serotype 2a; MEDLINE=22590274; PubMed=12704152; DOI=10.1128/IAI.71.5-2775-2786.2003; Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W., Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A., Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.R., "Complete genome sequence and comparative genomics of <i>Shigella flexneri</i> serotype 2a, strain 2457T"; Infect. Immun. 71:2775-2786 (2003).				
CC NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].				
RC SPRAIN-2457T / ATCC 700930 / Serotype 2a; MEDLINE=22590274; PubMed=12704152; DOI=10.1128/IAI.71.5-2775-2786.2003; Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W., Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A., Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.R., "Complete genome sequence and comparative genomics of <i>Shigella flexneri</i> serotype 2a, strain 2457T"; Infect. Immun. 71:2775-2786 (2003).				
CC CONVERTS the first step in hexosamine metabolism, converting fructose-6P into glucosamine-6P using glutamine as a nitrogen source (By similarity). L-glutamine + D-fructose 6-phosphate = L-glutamate + D-glucosamine 6-phosphate.				
CC SUBCELLULAR LOCATION: Cytoplasm (By similarity). SIMILARITY: In the C-terminal section; belongs to the SIS family.				
CC GFAKLGDSLIEHDIVHGLQALPSIEQM; SDRIBALAEEDSDRKHAFYGRGDQYPIAL 481				
DB 421 RKGLDASIEHDIVHGLQALPSIEQM; SDRIBALAEEDSDRKHAFYGRGDQYPIAL 480				
CC EGALKLGDSLIEHDIVHGLQALPSIEQM; SDRIBALAEEDSDRKHAFYGRGDQYPIAL 481				
DB 482 EGALKLGDSLIEHDIVHGLQALPSIEQM; SDRIBALAEEDSDRKHAFYGRGDQYPIAL 480				
CC EGALKLGDSLIEHDIVHGLQALPSIEQM; SDRIBALAEEDSDRKHAFYGRGDQYPIAL 481				
DB 481 EGALKLGDSLIEHDIVHGLQALPSIEQM; SDRIBALAEEDSDRKHAFYGRGDQYPIAL 480				
CC 542 GOLYVFAEQAQGFVSSDNMHIEMPHVEETAPIFYTVPLQLLAYVALKGTDVDQPRN				

Db	541. GOLYVFAODDAGFVSSDNMHIIMPHVEVIAPIFYTVPLQLLAYHVALIKSTDVDQPRN 600	Db	241. YDAGDKGTYRHMQKEIYEQNAIKNTLGRISHGQVDSLSEGPNADELLSKVEHIIQILA 300
Qy	602. LAKSVTVE 609	Qy	301. CGTYSNMGMSRYWFFSLAGPCDVIEASPYRISAVRNSLMTLSQSETADTLAGL 360
Db	601. LAKSVTVE 608	Db	301. CGTYSNMGMSRYWFFSLAGPCDVIEASPYRISAVRNSLMTLSQSETADTLAGL 360
RESULT 7		Qy	361. RLSKEIYLGLSLAICNPGSSLVRESDLALMTNAGTEIGVASTRAKFTTQLTVLMMVAKL 420
Q1YVN3_ SHISS PRELIMINARY; PRT; 609 AA.		Db	361. RLSKEIYLGLSLAICNPGSSLVRESDLALMTNAGTEIGVASTRAKFTTQLTVLMMVAKL 420
AC Q1YVN3;		Qy	421. SRLKGIDASIEBDIVGLQALSPRIEQLMSDKRTEALABEDSFDRKHAFLGRGDQPIA 480
DT 27-SEP-2005, integrated into UniProtKB/Trembl.		Db	421. SRLKGIDASIEBDIVGLQALSPRIEQLMSDKRTEALABEDSFDRKHAFLGRGDQPIA 480
DT 27-SEP-2005, sequence version 1.		Qy	481. LEGALKIKEISYHAAAYAAGELKHGQPLAJIDAMPVIVIAPNNELLEKLKSNIIEVRAR 540
DE L-glutamine:D-fructose-6-phosphate aminotransferase.		Db	481. LEGALKIKEISYHAAAYAAGELKHGQPLAJIDAMPVIVIAPNNELLEKLKSNIIEVRAR 540
GN Name=glns; OrderedLocusName=SSG_3899; ORFNames=SSO_3899;		Qy	541. GQOLYVADQDAGFVSDNNHIIEMPHVEETAPIFYTVPLQLLAYHVALIKGTDVDQPR 600
OS Shigella sonnei (strain Ss1).		Db	541. GQOLYVADQDAGFVSDNNHIIEMPHVEETAPIFYTVPLQLLAYHVALIKGTDVDQPR 600
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC Enterobacteriaceae; Shigellaceae.			
OX NCBI_TaxID=300269;			
RN [1]			
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].			
RX PubMed=162986; DOI=10.1033/nar/gk1954;			
RA Yang F., Yang J., Zhang X., Chen L., Jiang Y., Yan Y., Tang X., Wang J., Xiong Z., Dong J., Xue Y., Zhu Y., Xu X., Sun L., Chen S., Nie H., Peng J., Xu J., Wang Y., Yuan Z., Wen Y., Yao Z., Shen Y., Qiang B., Hou Y., Yu J., Jin O.;		Qy	601. NLAKSYTVE 609
RT "Genome dynamics and diversity of <i>Shigella</i> species, the etiologic agents of bacillary dysentery.";		Db	601. NLAKSYTVE 609
RT Nucleic Acids Res. 33:6445-6458(2005).			
RL			
CC Copyright by the UniProt Consortium, see http://www.uniprot.org/terms		RESULT 8	
CC Distributed under the Creative Commons Attribution-NoDerivs License		ID GLMS_ECOL6	
CC EMBL; CP00038; AA290429.1; -; Genomic_DNA.		ID GLMS_ECOL6	STANDARD;
CC DR GO:0005737; C:cytoplasm; IEA.		AC Q8FBF4;	PRT;
CC DR GO:0004160; F:glutamine-fructose-6-phosphate transaminase. . . ; IEA.		DT 06-JUN-2003, integrated into UniProtKB/Swiss-Prot.	
CC DR GO:0005739; F:sugar binding; IEA.		DT 06-JUN-2003, sequence version 2.	
CC DR GO:0016740; F:transferase activity; IEA.		DT 07-MAR-2006, entry version 17.	
CC DR GO:0016051; P:carbohydrate biosynthesis; IEA.		DE Glucosamine-fructose-6-phosphate aminotransferase (isomerizing)	
CC DR GO:0005975; P:metabolism; IEA.		DB (EC 2.6.1.16) (Hexosephosphate aminotransferase) (D-fructose-6-phosphate amidotransferase) (GFAT) (L-Glutamine-D-fructose-6-phosphate synthase).	
CC DR GO:0008152; P:metabolism; IEA.		DE amidotransferase (Glucosamine-6-phosphate synthase).	
CC InterPro: IPR000583; GATase_2.		GN Name=glmS; OrderedLocusName=c4654;	
CC InterPro: IPR000585; GATase_2.		OS Escherichia coli O1.	
CC InterPro: IPR000585; GATase_2.		OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	
CC InterPro: IPR001347; GImS_trans.		OC Enterobacteriaceae; Escherichia.	
DR Pfam; PF00310; GATase_2; 1.		NCBI_TaxID=217992;	
DR PIGRFAMs; TIGR01135; gImS; 1.		RN [1]	
DR PROSITE; PS00443; GATASE_TYPE_II; UNKNOWN_1.		RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	
KW Aminotransferase; Complete_proteome; Transferase.		RC STRAIN=06_H1 / CFT013 / ATCC 700928 / UPEC;	
SEQUENCE 609 AA; 66844 MW; 9BE71125CD34894 CRC64;		RC MEDLINE=22388234; Pubmed=12471157; DOI=10.1033/phas.25229799;	
DR		RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,	
DR		RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D., Mayhew G.F., Rose D.J., Zhou S.-Y., Schwartz D.C., Perna N.T.,	
DR		RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.,	
DR		RA RT "Extracellular mosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coli."	
DR		RT RT of uropathogenic Escherichia coli.	
DR		RT Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).	
DR		CC -1- FUNCTION: Catalyzes the first step in hexosamine metabolism, converting fructose-6-P into glucosamine-6-phosphate = L-	
DR		CC -1- nitrogen source (By similarity).	
DR		CC -1- CATALYTIC ACTIVITY: L-glutamine + D-fructose 6-phosphate.	
DR		CC -1- GLutamate + D-Glucosamine 6-phosphate.	
DR		CC -1- SUBUNIT: Homodimer (By similarity).	
DR		CC -1- SUBCELLULAR LOCATION: Cytoplasm (By similarity).	
DR		CC -1- SIMILARITY: In the C-terminal section, belongs to the SIS family.	
DR		CC -1- GFAT subfamily.	
DR		CC -1- SIMILARITY: Contains 1 type-2 glutamine amidotransferase domain.	
DR		CC Copyright by the UniProt Consortium, see http://www.uniprot.org/terms	
DR		CC Distributed under the Creative Commons Attribution-NoDerivs License	
DR		CC EMBL; A016769; AACN83086.1; -; Genomic_DNA.	
DR		DR HSSP; P12169; 1 MOS.	
DR		DR SMR; Q8FBF4; 1-239, 243-608.	
DR		DR GenomeReviews; A014075_GR; c4654.	
Qy			

DR	Biocyc; ECOL199310;C4654-MONOMER; -.	DT	30-AUG-2005, integrated into UniProtKB/Swiss-Prot.
DR	HANAP; MF_00164; -; 1.	DT	30-AUG-2005, sequence version 2.
DR	InterPro; IPR000563; GATase 2.	DT	07-MAR-2006, entry version 12.
DR	InterPro; IPR005885; GIMS_Trans.	DE	Glucosamine-fructose-6-phosphate aminotransferase [isomerizing]
DR	InterPro; IPR001347; SIS.	DE	(BC 2.6.1.16) (Hexosaminophosphate aminotransferase) (D-fructose-6-phosphate amidotransferase) (GATAT) (L-glutamine-D-fructose-6-phosphate amidotransferase) (Glucosamine-6-phosphate synthase).
DR	PFam; PF00310; GATase 2; 1.	DE	Name=gIMS; OrderedNames=SPA3700;
DR	TIGRFAMS; TIGR0135; gIMS; 1.	GN	Salmonella paratyphi-a.
DR	PROSITE; PS00443; GATASE_TYPE_II; 1.	OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
KW	Aminotransferase; Complete proteome; Glutamine amidotransferase;	OC	Enterobacteriaceae; Salmonella.
KW	Transfase.	OC	NCBI_TaxID=54388;
FT	INIT_MER 0 0	RN	NCBI_TaxID=54388;
FT	CHAIN 1 608	RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
FT		RC	STRAIN=ATCC 9150 / SARB42;
FT		RX	PubMed:15531082; DOI=10.1038/ng1470;
FT	REGION 1 240	RA	McClelland M., Sanderson K.E., Clifton S.W., Latrelle P., Porwollik S., Sabo A., Meyer R., Bieri T., Ozersky P., Harkins C.R., Wang C., Nguyen C., Berghoff A., Elliott G., Kohlberg S., Strong C., Du P., Carter J., Kremzki C., Leonard S., Sun H., Fulton L., Nash W., Miner T., Minx P., Delehaunty K., Fronick C., Magrini V., Nhan M., Warren W., Fiorea L., Spieh J., Wilson R.K.,
FT	ACT_SITE 1 603	RA	"Comparison of genome degradation in <i>Paratyphi A</i> and <i>Typhi</i> , human-pathogenic serovars of <i>Salmonella enterica</i> that cause typhoid.";
FT	ACT_SITE 603 AA; 66647 MW;	RL	RT Nat. Genet. 36:1268-1274 (2004).
SQ	SEQUENCE 608 AA;	CC	FUNCTION: Catalyzes the first step in hexosamine metabolism, converting fructose-6P into glucosamine-6P using glutamine as a nitrogen source (By similarity).
Query	Match 2	CC	-i- CATALYTIC ACTIVITY: L-glutamine + D-fructose 6-phosphate = L-glutamate + D-glucosamine 6-phosphate.
Query	Best Local Similarity 99.4%; Score 3067; DB 1; Length 608; Matches 605; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	CC	-i- SUBCELLULAR LOCATION: Cytoplasm (By similarity).
Db	CGIVGATAQDVAEILLEGLRRLERYGDSAGLAVIDDAEGHMTRIRRLGKVQMLAQAAE 61	CC	-i- SIMILARITY: In the C-terminal section; belongs to the SIS family.
Db	CGIVGATAQDVAEILLEGLRRLERYGDSAGLAVIDDAEGHMTRIRRLGKVQMLAQAAE 60	CC	GRAT subfamily.
Query	62 HPLHGGTGIAHTWATHGGPSEYNAHPVSEHVVVNGIENHEPLREALKRGTFVS 121	CC	-i- SIMILARITY: Contains 1 type-2 glutamine amidotransferase domain.
Db	61 HPLHGGTGIAHTWATHGGPSEYNAHPVSEHVVVNGIENHEPLREALKRGTFVS 120	CC	CC
Query	122 ETDTEVIAHLYVNLKOGGTLREAVLRAIPOLRGAYGTIVMDSRHPTDLAARSGSPLV 181	CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Db	121 ETDTEVIAHLYVNLKOGGTLREAVLRAIPOLRGAYGTIVMDSRHPTDLAARSGSPLV 180	CC	Distributed under the Creative Commons Attribution-NonDerivs License
Query	182 GLGMGENFTASDOLALLPVTTRRFITLEGGDIAFTRRVSNIIFDTKGAEVKRDIESNLQY 241	CC	CC
Db	181 GLGMGENFTASDOLALLPVTTRRFITLEGGDIAFTRRVSNIIFDTKGAEVKRDIESNLQY 240	CC	DR EMBL; CP000026; AAV79492.1; -; Genomic_DNA.
Query	242 DAGDKGTYRHYMKKEIVEQPNAIKNTLTGRISHQDVLSELGPNADELLSKYHQLAC 301	DR	DR SGR; SPKV9; 1-239; 243-608.
Db	241 DAGDKGTYRHYMKKEIVEQPNAIKNTLTGRISHQDVLSELGPNADELLSKYHQLAC 300	DR	DR Genomereviews; CP000026_GR; SPA3700.
Query	302 GTSYNSGKMSVRYMFESTLAGIPCDVEIASEFERYKSAVRRNSLIMTLSQGETADTLGLR 361	DR	DR HAMP; MF_00164; -; 1.
Db	301 GTSYNSGKMSVRYMFESTLAGIPCDVEIASEFERYKSAVRRNSLIMTLSQGETADTLGLR 360	DR	DR InterPro; IPR005838; GATase_2.
Query	362 LSKELGYLGSLALCNVPGSSLYRESDLALMTNNGTEGVASTKAFTQTLVLMVAKLS 421	DR	DR InterPro; IPR005855; GATMS_trans.
Db	361 LSKELGYLGSLALCNVPGSSLYRESDLALMTNNGTEGVASTKAFTQTLVLMVAKLS 420	DR	DR InterPro; IPR001347; SIS.
Query	482 EGALKLKRSYTHAEYAGELRKHGPLALIDADMPIVTVAPNNELEKLKSNEEYARG 541	DR	DR Pfam; PF00310; GATase_2; 1.
Db	481 EGALKLKRSYTHAEYAGELRKHGPLALIDADMPIVTVAPNNELEKLKSNEEYARG 540	DR	DR TIGRFAMS; TIGR0135; gIMS; 1.
Query	542 GOLYVFADQDAGFVSSDMMH1EMPHYBVIAPFYTPTPLQLLAYHVALKGTDVOPRN 601	DR	DR PROSITE; PS00443; GATASE_TYPE_II; 1.
Db	541 GOLYVFADQDAGFVSSDMMH1EMPHYBVIAPFYTPTPLQLLAYHVALKGTDVOPRN 600	DR	DR Aminotransferase; Complete_proteome; Glutamine amidotransferase; KW Transferase.
Query	612 RLKGLDASIEIDIVHGLQALPSRLEQMLSDKRIEALADFSDKHHALFLRGDQYPIAL 481	FT	FT INIT_MET 0 0 By similarity.
Db	421 RLKGLDASIEIDIVHGLQALPSRLEQMLSDKRIEALADFSDKHHALFLRGDQYPIAL 480	FT	FT CHAIN_N 1 608 Glucosamine-fructose-6-phosphate aminotransferase [isomerizing].
Query	482 EGALKLKRSYTHAEYAGELRKHGPLALIDADMPIVTVAPNNELEKLKSNEEYARG 541	FT	FT ACT_SITE 1 1 FT ACT_SITE 1 1 FT REGION 1 240 FT ACT_SITE 1 1 FT ACT_SITE 1 1 FT SEQUENCE 608 AA; 66719 MW; By similarity.
Db	481 EGALKLKRSYTHAEYAGELRKHGPLALIDADMPIVTVAPNNELEKLKSNEEYARG 540	FT	FT SEQUENCE 608 AA; 66719 MW; Isomerase (By similarity).
Query	542 GOLYVFADQDAGFVSSDMMH1EMPHYBVIAPFYTPTPLQLLAYHVALKGTDVOPRN 601	FT	FT REGION 1 240 FT SEQUENCE 608 AA; 66719 MW; Glutamine amidotransferase.
Db	541 GOLYVFADQDAGFVSSDMMH1EMPHYBVIAPFYTPTPLQLLAYHVALKGTDVOPRN 600	FT	FT SEQUENCE 608 AA; 66719 MW; Isomerase (By similarity).
Query	612 LAKSVTVE 609	FT	FT SEQUENCE 608 AA; 66719 MW; Glutamine amidotransferase.
Db	601 LAKSVTVE 608	FT	FT SEQUENCE 608 AA; 66719 MW; Glutamine amidotransferase.
RESULT 9			
ID	GIMS SALPA	STANDARD;	PRT; 608 AA.
AC	QSPKV9;		
RESULT 10			
Qy	2 CGIVGATAQRDVAEILLEGLRRLERYGDSAGLAVIDDAEGHMTRRLGKVQMLAQAAE 61	2	2 CGIVGATAQRDVAEILLEGLRRLERYGDSAGLAVIDDAEGHMTRRLGKVQMLAQAAE 61
Db	1 CGIVGATAQRDVAEILLEGLRRLERYGDSAGLAVIDDAEGHMTRRLGKVQMLAQAAE 60	1	1 CGIVGATAQRDVAEILLEGLRRLERYGDSAGLAVIDDAEGHMTRRLGKVQMLAQAAE 60
RESULT 11			
Qy	62 HPLHGGTGIAHTWATHGGPSEYNAHPVSEHVVVNGIENHEPLREALKRGTFVS 121	62	62 HPLHGGTGIAHTWATHGGPSEYNAHPVSEHVVVNGIENHEPLREALKRGTFVS 120
Db	61 HPLHGGTGIAHTWATHGGPSEYNAHPVSEHVVVNGIENHEPLREALKRGTFVS 120	61	61 HPLHGGTGIAHTWATHGGPSEYNAHPVSEHVVVNGIENHEPLREALKRGTFVS 120

Qy	122	ETDTEVIAHLVNWELKQGGTLREAVLRAAPQLRGAYGTIVMDSRHPDTLLAARSQSPLV 181	DR	InterPro; IPR005855; GluS_trans.
Db	121	ETDTEVIAHLVNWELKQGGTLREAVLRAAPQLRGAYGTIVMDSRHPDTLLAARSQSPLV 180	DR	InterPro; IPR01347; SIS_
Qy	182	GLGMGENFIASDOLALLPVRFLFEEGDIETTRRSVNFIFGTGAEVKRODIESNLQY 241	DR	InterPro; IPR01010; GATase_2;
Db	181	GLGMGENFIASDOLALLPVRFLFEEGDIETTRRSVNFIFGTGAEVKRODIESNLQY 240	DR	PFam; PF01380; SIS_
Qy	242	DAGKGKJYRHMOKEIYEQPNAIKNTLGPBISHQVQDLSLEIGNADELLSKVHIIQLAC 301	DR	TIGRFAMS; TIGR01135; GluS_1.
Db	241	DAGKGKJYRHMOKEIYEQPNAIKNTLGPBISHQVQDLSLEIGNADELLSKVHIIQLAC 300	DR	Aminotransferase; PS00443; GATase_TYPE_II; UNKNOWN_1.
Qy	302	GTSNSGMNSRYWPESSLAGIPCDVEIASPFYRKSAVERSIMITLSQSGETADTLAQLR 361	DR	Complete proteome; Transferase.
Db	301	GTSNSGMNSRYWPESSLAGIPCDVEIASPFYRKSAVERSIMITLSQSGETADTLAQLR 360	DR	SEQUENCE 609 AA; 66849 MW; E1D1FF6F1AF35F5C CRC64;
Qy	362	LSKELGYLGLSIAICNPGSSLVRESDLALMTNAGTEIGVASTAKFTTOLTVLMLYAKLS 421	Qy	Query Match 99.1%; Score 3058; DB 2; Length 609;
Db	361	LSKELGYLGLSIAICNPGSSLVRESDLALMTNAGTEIGVASTAKFTTOLTVLMLYAKLS 420	Qy	Best Local Similarity 98.9%; Pred. No. 1. 6e-184;
Qy	422	RLKGIDASLEHDIVHGQJALPSRTEQMLSQDKRTEALAEFDSDKHHALFLGRGDQYIAL 481	Db	Matches 602; Conservative 3; Mismatches 4; Indels 8 0; Gaps 0;
Db	421	RLKGIDASLEHDIVHGQJALPSRTEQMLSQDKRTEALAEFDSDKHHALFLGRGDQYIAL 480	Qy	1 MCGIVSIAQDVAEILLEGLRRLRZRGYDOSAGLAVVDAGHMTRRLRGKVMQLAQAAE 60
Qy	482	EGALKLKEIYSIHAAYAEGELKHGPALIADAMPPVYVAPNNELEKLKSNIEYARG 541	Db	1 MCGIVSIAQDVAEILLEGLRRLRZRGYDOSAGLAVVDAGHMTRRLRGKVMQLAQAAE 60
Db	481	EGALKLKEIYSIHAAYAEGELKHGPALIADAMPPVYVAPNNELEKLKSNIEYARG 540	Qy	61 EHPLHGGTGLAHTRWAHTGESEVNAHPHYSSEHTIVVHNGTILEHPLREELKARGYTGV 120
Qy	542	GQYVFAADDQDGIVSSDNNHHIEMPHVEVIAPIFYTVPLQLLAYVALKGSTDVQDPRN 601	Db	61 EHPLHGGTGLAHTRWAHTGESEVNAHPHYSSEHTIVVHNGTILEHPLREELKARGYTGV 120
Db	541	GQYVFAADDQDGIVSSDNNHHIEMPHVEVIAPIFYTVPLQLLAYVALKGSTDVQDPRN 600	Qy	1 MCGIVSIAQDVAEILLEGLRRLRZRGYDOSAGLAVVDAGHMTRRLRGKVMQLAQAAE 60
Qy	602	LAKSVTVE 609	Db	1 MCGIVSIAQDVAEILLEGLRRLRZRGYDOSAGLAVVDAGHMTRRLRGKVMQLAQAAE 60
Db	601	LAKSVTVE 608	Qy	1 MCGIVSIAQDVAEILLEGLRRLRZRGYDOSAGLAVVDAGHMTRRLRGKVMQLAQAAE 60
<hr/>				
RESULT 1.0				
Q5THY2_	SALCH	PRELIMINARY; PRT; 609 AA.	Qy	1 MCGIVSIAQDVAEILLEGLRRLRZRGYDOSAGLAVVDAGHMTRRLRGKVMQLAQAAE 60
AC	Q5THY2;		Db	1 MCGIVSIAQDVAEILLEGLRRLRZRGYDOSAGLAVVDAGHMTRRLRGKVMQLAQAAE 60
DT	10-MAY-2005,	integrated into UniProtKB/TREMBL.	Qy	1 MCGIVSIAQDVAEILLEGLRRLRZRGYDOSAGLAVVDAGHMTRRLRGKVMQLAQAAE 60
DT	10-MAY-2005,	sequence version 1.	Db	1 MCGIVSIAQDVAEILLEGLRRLRZRGYDOSAGLAVVDAGHMTRRLRGKVMQLAQAAE 60
DT	07-FEB-2006,	entry version 4.	Qy	1 MCGIVSIAQDVAEILLEGLRRLRZRGYDOSAGLAVVDAGHMTRRLRGKVMQLAQAAE 60
DB	L-glutamine-D-fructose-6-phosphate aminotransferase.		Db	1 MCGIVSIAQDVAEILLEGLRRLRZRGYDOSAGLAVVDAGHMTRRLRGKVMQLAQAAE 60
GN	Name=GluS; Order=locusName=SC3774; ORFNames=SC_3774;		Qy	1 MCGIVSIAQDVAEILLEGLRRLRZRGYDOSAGLAVVDAGHMTRRLRGKVMQLAQAAE 60
OS	Salmonella choleraesuis.		Db	1 MCGIVSIAQDVAEILLEGLRRLRZRGYDOSAGLAVVDAGHMTRRLRGKVMQLAQAAE 60
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;		Qy	1 MCGIVSIAQDVAEILLEGLRRLRZRGYDOSAGLAVVDAGHMTRRLRGKVMQLAQAAE 60
OX	Enterobacteriaceae; Salmonella.		Db	1 MCGIVSIAQDVAEILLEGLRRLRZRGYDOSAGLAVVDAGHMTRRLRGKVMQLAQAAE 60
RN	NCBI_TaxID=591;		Qy	1 MCGIVSIAQDVAEILLEGLRRLRZRGYDOSAGLAVVDAGHMTRRLRGKVMQLAQAAE 60
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].		Db	1 MCGIVSIAQDVAEILLEGLRRLRZRGYDOSAGLAVVDAGHMTRRLRGKVMQLAQAAE 60
STRAIN=SC-B677;			Qy	1 MCGIVSIAQDVAEILLEGLRRLRZRGYDOSAGLAVVDAGHMTRRLRGKVMQLAQAAE 60
RX	PubMed=1578495; DOI=10.1093/nar/gkt297;		Db	1 MCGIVSIAQDVAEILLEGLRRLRZRGYDOSAGLAVVDAGHMTRRLRGKVMQLAQAAE 60
Chiu C.-H., Tang P.-C., Chu C., Hu S., Bao Q., Yu J., Chou Y.-Y., Wang H.-S., Lee Y.-S.,			Qy	1 MCGIVSIAQDVAEILLEGLRRLRZRGYDOSAGLAVVDAGHMTRRLRGKVMQLAQAAE 60
RA	"The genome sequence of <i>Salmonella enterica</i> serovar <i>Choleraesuis</i> , a highly invasive and resistant zoonotic pathogen.";		Db	1 MCGIVSIAQDVAEILLEGLRRLRZRGYDOSAGLAVVDAGHMTRRLRGKVMQLAQAAE 60
RT	RT		Qy	1 MCGIVSIAQDVAEILLEGLRRLRZRGYDOSAGLAVVDAGHMTRRLRGKVMQLAQAAE 60
RL	Nucleic Acids Res. 33:1690-1698 (2005).		Db	1 MCGIVSIAQDVAEILLEGLRRLRZRGYDOSAGLAVVDAGHMTRRLRGKVMQLAQAAE 60
CC	Copyright by the UniProt Consortium, see http://www.uniprot.org/terms		Qy	1 MCGIVSIAQDVAEILLEGLRRLRZRGYDOSAGLAVVDAGHMTRRLRGKVMQLAQAAE 60
CC	Distributed under the Creative Commons Attribution-NoDerivs License		Db	1 MCGIVSIAQDVAEILLEGLRRLRZRGYDOSAGLAVVDAGHMTRRLRGKVMQLAQAAE 60
DR	EMBL; AB017220; AA67680_1; -; Genomic_DNA.		Qy	1 MCGIVSIAQDVAEILLEGLRRLRZRGYDOSAGLAVVDAGHMTRRLRGKVMQLAQAAE 60
PC	NCBI; Q5THY2; 2-240; 244-609.		Db	1 MCGIVSIAQDVAEILLEGLRRLRZRGYDOSAGLAVVDAGHMTRRLRGKVMQLAQAAE 60
SNR	Q5THY2;		Qy	1 MCGIVSIAQDVAEILLEGLRRLRZRGYDOSAGLAVVDAGHMTRRLRGKVMQLAQAAE 60
DR	GO; GO:005737; C:cycloplasm; IEA.		Db	1 MCGIVSIAQDVAEILLEGLRRLRZRGYDOSAGLAVVDAGHMTRRLRGKVMQLAQAAE 60
DR	GO; GO:004360; F:glutamine-fructose-6-phosphate transaminase. . . IEA.		Qy	1 MCGIVSIAQDVAEILLEGLRRLRZRGYDOSAGLAVVDAGHMTRRLRGKVMQLAQAAE 60
DR	GO; GO:0005529; F:sugar binding; IEA.		Db	1 MCGIVSIAQDVAEILLEGLRRLRZRGYDOSAGLAVVDAGHMTRRLRGKVMQLAQAAE 60
DR	GO; GO:016740; F:transferase activity; IEA.		Qy	1 MCGIVSIAQDVAEILLEGLRRLRZRGYDOSAGLAVVDAGHMTRRLRGKVMQLAQAAE 60
DR	GO; GO:0016051; P:carbohydrate biosynthesis; IEA.		Db	1 MCGIVSIAQDVAEILLEGLRRLRZRGYDOSAGLAVVDAGHMTRRLRGKVMQLAQAAE 60
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.		Qy	1 MCGIVSIAQDVAEILLEGLRRLRZRGYDOSAGLAVVDAGHMTRRLRGKVMQLAQAAE 60
DR	GO; GO:0008152; P:metabolism; IEA.		Db	1 MCGIVSIAQDVAEILLEGLRRLRZRGYDOSAGLAVVDAGHMTRRLRGKVMQLAQAAE 60
DR	InterPro; IPR000583; GATase_2.		Qy	1 MCGIVSIAQDVAEILLEGLRRLRZRGYDOSAGLAVVDAGHMTRRLRGKVMQLAQAAE 60

OX	NCBI_TaxID=602;	Db	241 DAGDGKGIYRHMQKEIYEOPNAIKNTLGRISHQVDLSELGPNADELLSKVHIIQILAC 300
RP	NUCLEOTIDE SQUENCE [LARGE SCALE GENOMIC DNA].	Qy	302 GTSYNSGMVSYRNWPESSLACIPCDVYLASEFRRYRKSAYRNSLMITLSQGETADTLAGR 361
RC	STRAIN=LT2 / SGSC4142 / ATCC 700720;	Db	301 GTSYNSGMVSYRNWPESSLACIPCDVYLASEFRRYRKSAYRNSLMITLSQGETADTLAGR 360
RX	MEDLINE=2134348; PubMed=11038/35101614;	Qy	362 LSKEGLYGLS LAICNVPGSSLVRESDLALMTNAGTEIGVASTRAKFTTQLTVLMLVAKUS 421
RA	McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du P., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K., RT2,"	Db	361 LSKEGLYGLS LAICNVPGSSLVRESDLALMTNAGTEIGVASTRAKFTTQLTVLMLVAKUS 420
RA	Complete genome sequence of <i>Salmonella enterica</i> serovar <i>Typhimurium</i> Nature 413:852-855(2001).	Qy	422 RLKGKDASIEBDTIVHGLQALPSRIBQMLSQDKRIBELLAEDFSDKHHALPLGRGDQYPIAL 481
CC	converting fructose-6P into glucosamine-6P using glutamine as a nitrogen source (By similarity).	Db	421 RLKGKDASIEBDTIVHGLQALPSRIBQMLSQDKRIBELLAEDFSDKHHALPLGRGDQYPIAL 480
CC	-!- CATALYTIC ACTIVITY: L-glutamate + D-fructose 6-phosphate = L-glutamate + D-glucosamine 6-phosphate.	Qy	482 EGALKLKESIYHAYAAGELKHGPLAIDAMPVIVAPANNELLEKLKSNTIEBVRARG 541
CC	-!- SUBUNIT: Homodimer (By similarity).	Db	481 EGALKLKESIYHAYAAGELKHGPLAIDAMPVIVAPANNELLEKLKSNTIEBVRARG 540
CC	-!- SIMILARITY: Cycoplasm (By similarity).	Qy	542 GQLVPAADDAGFVSDNNHIIEMPHEVEVIAPFIFTYPLQLLAYHVALIKGTDVDQPRN 601
CC	-!- SIMILARITY: In the C-terminal section; belongs to the SIS family.	Db	541 GQLVPAADDAGFVSDNNHIIEMPHEVEVIAPFIFTYPLQLLAYHVALIKGTDVDQPRN 600
CC	GFAT subfamily. Contains 1 type-2 glutamine amidotransferase domain.	Qy	602 LAKSVTVE 609
CC	Copyright by the UniProt Consortium, see http://www.uniprot.org/terms	Db	601 LAKSVTVE 608
CC	Distributed under the Creative Commons Attribution-NoDerivs License		
DR	EMBL; A008880; ALI22719.1; -; Genomic_DNA.		RESULT 12
DR	HSSP; P1169; 1JXA.	GLMS_SALTI	GLMS_SALTI
DR	Q8RKK1; 1-239, 243-608.	ID	ID
DR	GenomeReviews; A0006468_GR; STM3861.	QB22_Q2	STANDARD; STANDARD;
DR	Biocyc; STYPP9287; STM3861-MONOMER; -.	AC	PRT; PRT;
DR	HAMAP; MP_00164; -; 1.	DT	608 AA.
DR	InterPro; IPR00583; Gtase 2.	DT	11-JUL-2002, integrated into UniProtKB/Swiss-Prot.
DR	InterPro; IPR00585; GLMS_Trans.	DT	11-JUL-2002, sequence version 2.
DR	InterPro; IPR01347; SIS_-	DT	07-MAR-2006, entry version 27.
DR	Pfam; PF01380; Gtase 2; 1.	DE	Glucosamine--fructose-6-phosphate aminotransferase (isomerizing)
DR	PFAM; PF01380; SIS 2_-	DE	(EC 2.6.1.16) (Hexosephosphate aminotransferase) (D-fructose-6-phosphate amidotransferase) (GFAT) (L-glutamate-D-fructose-6-phosphate amidotransferase) (Glucosamine-6-phosphate synthase).
DR	TIGRFAMS; TIGR0115; GmS; 1.	DE	Name=glnS; OrderedLocusNames=Str1917, t3638;
DR	PROSITE; PS00443; GATASE_TYPEII; 1.	GN	Salmonella typhi.
KW	Aminotransferase; Complete proteome; Glutamine amidotransferase; Transf erase.	OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Salmonella.
KW	INIT_MER 0 0	OC	NCB_ TaxID=601;
FT	CHAIN 1 608	OX	NCB_ TaxID=601;
FT		RN	[1]
FT		RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
FT		RC	STRAIN=CT18; MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
FT	REGION 1 240	RX	PA
FT	ACT_SITE 1 1	PA	PA
FT	ACT_SITE 603 603	PA	PA
SO	SEQUENCE 608 AA: 66746 MW: C320C718DEDAF52 CRC64;	PA	PA
Qy	99.0%; Score 3055; Pred. No. 2.5e-184; Matches 602; Conservative 2; Mismatches 4; Indels 0; Gaps 0;	PA	PA
Db	2 CGTYGAIAGORDVAELLEGARRLBYRGYDVSAGLAVDAAFGHMPTRARRYGKVMQLAQAE 61	PA	PA
Db	1 CGIVGAIAGORDVAELLEGARRLBYRGYDVSAGLAVDAAFGHMPTRARRYGKVMQLAQAE 60	PA	PA
Qy	62 HPLHGGTGIAHTRWATHGGESEVNAHAPHYSEHIVVYNGIENHEPLREKARYTYS 121	PA	PA
Db	61 HPLHGGTGIAHTRWATHGGESEVNAHAPHYSEHIVVYNGIENHEPLREKARYTYS 120	PA	PA
Qy	Best Local Similarity 99.0%; Pred. No. 2.5e-184; Matches 602; Conservative 2; Mismatches 4; Indels 0; Gaps 0;	PA	PA
Db	122 ETDTDEVIAVLNVWEKQGGLTREAVLTAIPQRLGAYGTIMDSRHPDTLIAARSGLPV 181	PA	PA
Qy	121 ETDTDEVIAVLNVWEKQGGLTREAVLTAIPQRLGAYGTIMDSRHPDTLIAARSGLPV 180	PA	PA
Db	182 GLGMGENFIASDOLALLPTTRRFLEKEDIAETTRRSYNTFDTKGAYKRDIESNLQY 241	PA	PA
Qy	181 GLGMGENFIASDOLALLPTTRRFLEKEDIAETTRRSYNTFDTKGAYKRDIESNLQY 240	PA	PA
Db	242 DAGDGKGIYRHMQKEIYEOPNAIKNTLGRISHQVDLSELGPNADELLSKVHIIQILAC 301	PA	PA

CC	Glutamate + D-glucosamine 6-phosphate.	Qy	482 EGALKKKEISYTHAEAYAAGBLKGLALIDADMPVIVVAPNNELEKLKSNTEEVYRARG 541
CC	- - SUBCELLULAR LOCATION: Cytoplasm (By similarity).	Db	481 EGALKKKEISYTHAEAYAAGBLKGLALIDADMPVIVVAPNNELEKLKSNTEEVYRARG 540
CC	- - SIMILARITY: In the C-terminal section, belongs to the SIS family.	Qy	542 GOLYVFDADQDGFSQSDNMMHITEMPVEEVAPIFYVPLQLLAYVALIKGTDVQPRN 601
CC	GFAT subfamily.	Db	541 GOLYVFSQDQDGFSQSDNMMHITEMPVEEVAPIFYVPLQLLAYVALIKGTDVQPRN 600
CC	- - SIMILARITY: Contains 1 type-2 glutamine amidotransferase domain.	Qy	602 LAKSVTVE 609
CC	Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms	Db	601 LAKSVTVE 608
CC	Copyrighted under the Creative Commons Attribution-NoDerivs License		
CC	EMBL: AL627280; CDD03134.1; ; Genomic DNA.		
DR	EMBL: AE014613; AP071155.1; ; Genomic DNA.		
DR	HSSP; P17159; IMOS.		
DR	Q822Q2; 1-231; 243-608.		
DR	GenomeReviews; AL013382; GR; STR1917.		
DR	GenomeReviews; AE014613; GR; t3658.		
DR	BioCyc; SENT0370; STY3917-MONOMER; -.		
DR	HANAP; MF_00164; ; 1.		
DR	InterPro; IPR000533; GATase 2.		
DR	InterPro; IPR005855; GlmS_trans.		
DR	InterPro; IPR01347; SIS.		
DR	PFAM; PF00310; GATase 2; 1.		
DR	PFAM; PF01380; SIS; 2.		
DR	TIGRFAMs; TIGR01135; glmS; 1.		
DR	PROSITE; PS00443; GATASE_TYPE_II; 1.		
KW	Amidotransferase; Complete proteome; Glutamine amidotransferase; Transferase.		
FT	INIT_MER 0		
FT	CHAIN 1	0 0	
FT	PTM 608		
FT	REGION ACT_SITE 1	240 1	
FT	ACT_SITE ACT_SITE 1 603	603 603	
SQ	SEQUENCE 3F18EABA47D4A804 CRC64;	66721 MW;	
Qy	98.8%; Score 3048; DB 1; Length 608;		
Matches	Best Local Similarity 98.5%; Pred. No. 78-184; RT		
Matches	5; Mismatches 4; Indels 0; RT		
Qy	2 CGIVGATIAQRDVAILLEGLRRLREYRGDSAGLAVVDAEGHMTRLRLGKVQMLAQAAE 61		
Db	1 CGIVGATIAQRDVAILLEGLRRLREYRGDSAGLAVVDAEGHMTRLRLGKVQMLAQAAE 60		
Qy	62 HPLHGGTCIAHTRWATGEPSYNAHPVSEHIVVHNGTENHEPARELKARGTYFVS 121		
Db	61 HPLHGGTCIAHTRWATGEPSYNAHPVSEHIVVHNGTENHEPARELKARGTYFVS 120		
Qy	122 ETDTEVIAHLVWELKGQGTLEAVRLAIPOQGAVGTVIDSRHDPTLAAARSGLPV 181		
Db	121 ETDTEVIAHLVWELKGQGTLEAVRLAIPOQGAVGTVIDSRHDPTLAAARSGLPV 180		
Qy	182 GLGMGENPIASDQLALLPVTTRRFIFLEGIDAEITRRSVNIFDKTGAEVKRQDIESNLQY 241		
Db	181 GLGMGENPIASDQLALLPVTTRRFIFLEGIDAEITRRSVNIFDNTGAEVKRQDIESNLQY 240		
Qy	242 DAGDKGYRHYMOKETIEVQPNIAKNTLGRISHQGYDLSLEGPNADELLSKVHQLAC 301		
Db	241 DAGDKGYRHYMOKETIEVQPNIAKNTLGRISHQGYDLSLEGPNADELLSKVHQLAC 300		
Qy	302 GTSYNSGMVSRVWFESELAGIPCDVEASEFVRSKAVRNSLMTLSQSETADLAGR 361		
Db	301 GTSYNSGMVSRVWFESELAGIPCDVEASEFVRSKAVRNSLMTLSQSETADLAGR 360		
Qy	362 LSKELGIGLSLACIYNPGSLSYRESDLALMTNAGTEIGVASTKRAFTQTLVLMVAKLS 421		
Db	361 LSKELGIGLSLACIYNPGSLSYRESDLALMTNAGTEIGVASTKRAFTQTLVLMVAKLS 420		
Qy	422 RUKGLDASIEHDIVHGLQALPERIEQMLSDQRKRIEALAEFSDKHFALEGRGDOYPIAL 481		
Db	421 RUKGLDASIEHDIVHGLQALPSRQEMLSDQRKRIEALAEFSDKHFALEGRGDOYPIAL 480		

FT	REGION	1	241	Glutamine amidotransferase.
FT	ACT SITE	1	1	GATase (By similarity).
FT	ACT SITE	604	604	Isomerization Fru-6P (By similarity).
SQ	SEQUENCE	609 AA;	66668 MW;	BEE718EDFD2385D CRC64;
Query Match	Best Local Similarity	86.9%;	Score 2681.5-;	DB 1; Length 609;
	Matches 51.8%;	Conservative	85.1%;	Pred. No. 1e-160;
Qy	2	CGIVGAIAGRDVAILLESLRRLERGYSAGLAVYDAGFHMTRLRRGKVQMLAQAAE	61	1; Gaps 1;
Db	1	CGIVGAVAGRDVAILLESLRRLERGYSAGLAVYDAGFHMTRLRRGKVQMLAQAAE	60	[2];
Qy	62	HPLHGGTGAAHTRWATHGGSPEVNAHPHYSSEHIVVANGIENEPBLAKRGYTFVS	121	RN
Db	61	HELHGGTGAAHTRWATHGGSPEVNAHPHYSSEHIVVANGIENEPBLAKRGYTFVS	120	RX
Qy	122	ETDTEVIAHLVNLWKLQ-GGTLRBAVLRAIPQRGAYGTVIMDSRHPDTLLAARSQSPLV	180	RC
Db	121	ETDTEVIAHLVNLWKLQ-GGTLRBAVLRAIPQRGAYGTVIMDSRHPDTLLAARSQSPLV	180	RX
Qy	181	IGLGMGENITASDQLAI,PTVTRTEFLFEGDIAITRTRSVNIDTKTGAEVKRDQIESNQ	240	RX
Db	181	IGRGVGENITASDQLAI,PTVTRTEFLFEGDIAITRTRSVNIDTKTGAEVKRDQIESNQ	240	RN
Qy	241	YDADKGK1RHYMOKEIYEPNALKNTLGRISHQVDSLGPNAELLSKVEH1QILQ	300	RX
Db	241	YDADKGK1RHYMOKEIYEPNALKNTLGRISHQVDSLGPNAELLSKVEH1QILQ	300	RC
Qy	301	CGTNSYNSGRVSRWYFESLAGIPCDVIAESEFRYRKSAYVRNSLIMTISQSGETADTLAGL	360	RX
Db	301	CGTNSYNSGRVSRWYFESLAGIPCDVIAESEFRYRKSAYVRNSLIMTISQSGETADTLA	360	RC
Qy	361	RLSKELGIGLSSLAINCVNPOSSLVRESDLALMTNAGTEGGVASTKAFTTQTLVILMLYAKL	420	RX
Db	361	RLSKELGIGLSSLAINCVNPOSSLVRESDLALMTNAGTEGGVASTKAFTTQTLVILMLYARV	420	RC
Qy	421	SRLKGLDASIEHDIVGLALPSRQEMQSQDRIEALEDFSKDHAKFLGRGDQPIA	480	RX
Db	421	GRLRGMDAQIEHDIVHGLCALPARIEQMSQDQKIESLAEGFSDKDHAKFLGRGDQPIA	480	RC
Qy	481	LEGALKLKRISYIHAAYAAGELKGHPGLLADMPVTVAPNELLKLKSNIEEVRAR	540	RX
Db	481	MEAGKLKRISYIHAAYAAGELKGHPGLLADMPVTVAPNELLKLKSNIEEVRAR	540	RC
Qy	541	GGOLLYVPAODAGTVSSDNMHIEMPHYEVIAPIFYTVPLQLAYVALIKSTDVQPR	600	RX
Db	541	GGELYVPAODAGTVSSDNMHIEMPHYEVIAPIFYTVPLQLSYHVALIKSTDVQPR	600	RC
Qy	601	NLAKSVTVE	609	RX
Db	601	NLAKSVTVE	609	RC
RESULT 14	GLMS_YERPE	STANDARD;	PRT;	608 AA.
AC	Q82958;			
DT	11-JUL-2002,	integrated into UniProtKB/Swiss-Prot.		
DT	11-JUL-2002,	sequence version 2.		
DT	07-MAR-2006,	entry version 32.		
DB	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]			
DE	(EC 2.6.1.16) (Hexosephosphate aminotransferase) (D-fructose-6-			
DE	phosphate amidotransferase) (GFAT) (L-glutamine-D-fructose-6-			
DE	amidotransferase) (Glucosamine-6-phosphate synthase).			
GN	Name=GLMS; OrderedLocusName=YPO4118, Y4132, YPA025;			
OS	Yersinia pestis.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Yersinia.			
OX	NCB_TAXID=632;			
RN	[1] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].			
RC	STRAIN=CO-92 / Biovar Orientalis;			

PT	ACT SITE	603	603	Isomerization Fru-6P (By similarity).
SQ	SEQUENCE	608 AA;	66394 MN;	16E5FDADB16CCD6 CRC64;
Query Match		86.7%;	Score 2677;	DB 1; Length 608;
Best Local Similarity		85.0%;	Pred. No. 2e-160;	
Matches	517;	Conservative	44;	Mismatches 47; Indels 0; Gaps 0;
Qy	2	CGIVGAIARDVAELLEGRLRRLYRGYDGSAGLAVIDAEGHMTLRLRUGKVQMLAQAE 61		
Db	1	CGIVGAVARDIAELLEGRLRRLYRGYDGSAGLAVIDAEGHMTLRLRUGKVQMLAQAE 60		
Qy	62	HPLHGGTGTGAHTRWAHGPESEYNAHPHYSIETIVVINGIENIHEPLRELKARGYTFVS 121		
Db	61	QDLHGGTGTGAHTRWAHGPESEYNAHPHYSIETIVVINGIENIHEPLRELKARGYTFVS 120		
Qy	122	ETDPEVIAHLVNLWELKQGGLTREAVLRAPIPLQRLGAYTIVIMOSRHPDTLAAIRSGSPLV 181		
Db	121	ETDPEVIAHLVNLWELKQGGLTREAVLRAPIPLQRLGAYTIVIMOSRHPDTLAAIRSGSPLV 180		
Qy	182	GLGNGENFLASDQLALLPTVTRRFIFLEEDDIABITRRSVNIIFDTKGAEVKRODIESNLQY 241		
Db	181	GGVGENFLASDQLALLPTVTRRFIFLEEDDIABITRRSVNIIFDTKGAEVKRODIESNLQY 240		
Qy	242	DAGDKGIYHMHYMOKEIYEDPNAIKNTLGTGRISHGQVDLSELGPNADEELSKVHEHQLAC 301		
Db	241	DAGDKGIYHMHYMOKEIYEDPNAIKNTLGTGRISHGQVDLSELGPNADEELSKVHEHQLAC 300		
Qy	302	GTSYNSGMWSRYWPESLAGIPCOVETASERFRKSAVNRNSLMITLSQSGETADTLAQLR 361		
Db	301	GTSYNSGMWSRYWPESLAGIPCOVETASERFRKSAVNRNSLMITLSQSGETADTLAQLR 360		
Qy	362	LSEKLGYLSLATICNPVPGGSVLVRESDLALMTNAGTEIQCVASTAKFTIQLTVLMLVAKLS 421		
Db	361	LSEKLGYLSLATICNPVPGGSVLVRESDLALMTNAGTEIQCVASTAKFTIQLTVLMLVAKIG 420		
Qy	422	RLKOLDASIEHDIVGLLGLPSRTEQMLSQDKRIEALAEADFSDKHHALFLGRGDQYPIAL 481		
Db	421	RLKGDADASIEHDIVHALQLPARIEQMLSDKTEALAEQFSDKHHALFLGRGDQYPIAM 480		
Qy	482	EGALKLKEKSYIAYAAGELKHGPLALIDADMPIVIVAPNELLKLNKSNIEEVTRARG 541		
Db	481	EGALKLKEKSYIAYAAGELKHGPLALIDADMPIVIVAPNELLKLNKSNIEEVTRARG 540		
Qy	542	GQLYVFAQDAGPVSSDMWHILEPHVEVIAPIIYTVPQLQLAYVALIKGTVDQPRN 601		
Db	541	GQLYVFAQDAGPVSSDMWHILEPHVEVIAPIIYTVPQLQLAYVALIKGTVDQPRN 600		
Qy	602	LAKSVTVE 609		
Db	601	LAKSVTVE 608		
RESULT 15				
GMS_YERPS	ID	GMS_YERPS	STANDARD;	ERT;
	AC	Q663R1;		608 AA.
	DT	30-AUG-2005,	integrated into UniProtKB/Swiss-Prot.	
	DT	07-MAR-2006,	sequence version 2.	
	DE	Glucosamine-6-phosphate aminotransferase [isomerizing]		
	DE	(EC 2.6.1.16) (Hexosaminophosphate aminotransferase) (D-fructose-6-phosphate amidotransferase) (GAT) (L-glutamine-D-fructose-6-phosphate amidotransferase) (Glucosamine-6-phosphate synthase).		
	DE	Name=GIMS; OrdererdLocusNames=YTB3954;		
	OS	Yersinia pseudotuberculosis.		
	OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;		
	OC	Enterobacteriaceae; Yersinia.		
	NCBI_TaxID	633;		
RN	NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).			
RC	STRID:IP33953 / Serotype I;			
RX	PubMed:1539858; DOI=10.1073/pnas.040412101;			
RA	Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,			
RA	362 LSXELGLGSLAICNPVGSILYRESDLALMTNAGTEIQCVASTAKFTIQLTVLMLVAKLS 421			
RA	361 LSXELGLGSLAICNPVGSILYRESDLALMTNAGTEIQCVASTAKFTIQLTVLMLVGRIG 420			
RA	Regala W.M., Georgescu A.M., Vergez L.M., Lard M.L., Motin V.L.,			
RA	Brubaker R.R., Fowler J., Hinnebusch J., Marceau M., Medigue C.,			
RA	Simone M., Chenal-Francisque V., Souza B., Dacheux D., Elliott J.M.,			
RA	Derbise A., Hauser B.J., Garcia E.,			
RT	"Insights into the evolution of <i>Yersinia</i> pectins through whole-genome comparison with <i>Yersinia pseudotuberculosis</i> ,"			
RT	Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831 (2004).			
CC	-!- FUNCTION: Catalyzes the first step in hexosamine metabolism, a			
CC	converting fructose-6P into glucosamine-6P using glutamine as a			
CC	nitrogen source (By similarity).			
CC	-!- CATALYTIC ACTIVITY: L-glutamine + D-fructose-6-phosphate = L-			
CC	Glutamate + D-glucosamine 6-phosphate.			
CC	-!- SUBCELLULAR LOCATION: Cyttoplasm (By similarity).			
CC	-!- SIMILARITY: In the C-terminal section; belongs to the SIS family.			
CC	GAT subfamily.			
CC	-!- SIMILARITY: Contains 1 type-2 glutamine amidotransferase domain.			
CC	-!- nitrogen source (By similarity).			
CC	Copyright by the UniProt Consortium, see http://www.uniprot.org/terms			
CC	Distributed under the Creative Commons Attribution-NoDerivs License			
CC	EMBL: BX363987; CAR32302.1; -; Genomic_C_DNA.			
DR	SMR; Q663R1; 1-239, 243-608.			
DR	GenomeReviews: BX936398_GR; YPTB3954.			
DR	HAMAP; MF_00165;			
DR	InterPro: IPR005853; GATase_2.			
DR	InterPro: IPR005855; GATs_tTrans.			
DR	InterPro: IPR001347; SIS_Pfam.			
DR	PF00310; GATase_2.			
DR	PF01380; SIS_2.			
DR	TIGR405; TIGR01135; GIMS_1.			
DR	PROSITE: PS0043; GATASE_TYPE_II_1.			
KW	Aminotransferase; Complete Proteome; Glutamine amidotransferase;			
KW	Initiator.			
FT	INIT_MET			
FT	CHAIN			
FT	0			
FT	608			
FT	By similarity.			
FT	Glucosamine-6-phosphate aminotransferase (isomerizing).			
FT	/FRID=PRO_0000135419.			
FT	Glutamine amidotransferase.			
FT	GATase (By similarity).			
FT	Isomerization Fru-6P (By similarity).			
FT	Best Local Similarity 85.0%; Pred. No. 2e-160;			
FT	Matches 517; Conservative 44; Mismatches 47; Indels 0; Gaps 0;			
Qy	2 CGIVGAIARDVAELLEGRLRRLYRGYDGSAGLAVIDAEGHMTLRLRUGKVQMLAQAE 61			
Db	1 CGIVGAVARDIAELLEGRLRRLYRGYDGSAGLAVIDAEGHMTLRLRUGKVQMLAQAE 60			
Qy	62 HPLHGGTGTGAHTRWAHGPESEYNAHPHYSIETIVVINGIENIHEPLRELKARGYTFVS 121			
Db	61 QDLHGGTGTGAHTRWAHGPESEYNAHPHYSIETIVVINGIENIHEPLRELKARGYTFVS 120			
Qy	122 ETDPREVIAHLVNLWELKQGGLTREAVLRAPIPLQRLGAYTIVIMOSRHPDTLAAIRSGSPLV 181			
Db	121 ETDPEVIAHLVNLWELKQGGLTREAVLRAPIPLQRLGAYTIVIMOSRHPDTLAAIRSGSPLV 180			
Qy	182 GLGNGENFLASDQLALLPTVTRRFIFLEEDDIABITRRSVNIIFDTKGAEVKRODIESNLQY 241			
Db	181 GGGVGENFLASDQLALLPTVTRRFIFLEEDDIABITRRSVNIIFDTKGAEVKRODIESNLQY 240			
Qy	242 DAGDKGIYHMHYMOKEIYEDPNAIKNTLGTGRISHGQVDLSELGPNADEELSKVHEHQLAC 301			
Db	241 DAGDKGIYHMHYMOKEIYEDPNAIKNTLGTGRISHGQVDLSELGPNADEELSKVHEHQLAC 300			
Qy	302 GTSYNSGMWSRYWPESLAGIPCOVETASERFRKSAVNRNSLMITLSQSGETADTLAQLR 361			
Db	301 GTSYNSGMWSRYWPESLAGIPCOVETASERFRKSAVNRNSLMITLSQSGETADTLAQLR 360			
Qy	362 LSEKLGYLSLATICNPVPGGSVLVRESDLALMTNAGTEIQCVASTAKFTIQLTVLMLVAKLS 421			
Db	361 LSEKLGYLSLATICNPVPGGSVLVRESDLALMTNAGTEIQCVASTAKFTIQLTVLMLVAKIG 420			
Qy	422 RLKOLDASIEHDIVGLLGLPSRTEQMLSQDKRIEALAEADFSDKHHALFLGRGDQYPIAL 481			
Db	421 RLKGDADASIEHDIVHALQLPARIEQMLSDKTEALAEQFSDKHHALFLGRGDQYPIAM 480			
Qy	482 EGALKLKEKSYIAYAAGELKHGPLALIDADMPIVIVAPNELLKLNKSNIEEVTRARG 541			
Db	481 EGALKLKEKSYIAYAAGELKHGPLALIDADMPIVIVAPNELLKLNKSNIEEVTRARG 540			
Qy	542 GQLYVFAQDAGPVSSDMWHILEPHVEVIAPIIYTVPQLQLAYVALIKGTVDQPRN 601			
Db	541 GQLYVFAQDAGPVSSDMWHILEPHVEVIAPIIYTVPQLQLAYVALIKGTVDQPRN 600			
Qy	602 LAKSVTVE 609			
Db	601 LAKSVTVE 608			
Qy	608 AA.			
Db	608 AA.			
Qy	61 QDLHGGTGTGAHTRWAHGPESEYNAHPHYSIETIVVINGIENIHEPLRELKARGYTFVS 121			
Db	61 ETDPREVIAHLVNLWELKQGGLTREAVLRAPIPLQRLGAYTIVIMOSRHPDTLAAIRSGSPLV 180			
Qy	62 GLHGGENFLASDQLALLPTVTRRFIFLEEDDIABITRRSVNIIFDTKGAEVKRODIESNLQY 241			
Db	61 GCGYGENFLASDQLALLPTVTRRFIFLEEDDIABITRRSVNIIFDTKGAEVKRODIESNLQY 240			
Qy	62 DAGDKGIYHMHYMOKEIYEDPNAIKNTLGTGRISHGQVDLSELGPNADEELSKVHEHQLAC 301			
Db	61 DAGDKGIYHMHYMOKEIYEDPNAIKNTLGTGRISHGQMDSELGPNADEELSKVHEHQLAC 300			
Qy	630 GTSYNSGMWSRYWPESLAGIPCDVDEIASEFRYKSAVNRNSLMTLSQSGETADTLAQLR 361			
Db	630 GTSYNSGMWSRYWPESLAGIPCDVDEIASEFRYKSAVNRNSLMTLSQSGETADTLAQLR 360			

Qy 422 RLKGIDASIEHDIVGLOALPSRIBQMLSQDKRIBALAEFSDKHHALFLGRGDOYPTAL 481
Db 421 KLKGADASIEHDIVHALQQLPARTEQMLSLDKTEBALAFGFSDKHHALFLGRGDOYPTAM 480
Qy 482 EGALKLKE:SYIHAAYAAGELKGPLALI.DADMPIVIVAPNNELEKLSN1BEVRARG 541
Db 481 EGALKLKE:SYIHAAYAAGELKGPLALI.DADMPIVIVAPNNELEKLSN1BEVRARG 540
Qy 542 GQLYVFAODAGFVSSDNHHI1EMPHVEVIAPIFYTVPLQLLAYHVALIKGTDVDQPRN 601
Db 541 GQLYVFAODAGFTDSEGKIIQLPHVERIIAPIFYTVPLQLLSYHVALIKGTDVDQPRN 600
Qy 602 LAKSVTVE 609
Db 601 LAKSVTVE 608

Search completed: August 7, 2006, 09:24:37
Job time : 157 secs

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OM protein - protein search, using sw model

Run on: August 7, 2006, 09:25:52 ; Search time 24 Seconds

(without alignments)

2221.090 Million cell updates/sec

Title: US-10-612-779-2

Perfect score: 3086

Sequence: 1 MCGIVGAIAGORDVAILEG.....LIKGDVDQPRNLAKSVTVE 609

Scoring table: BLOSUM62

Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/baCfiless.pep:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Query	Description
1	3086	100.0	609	2	US-09-115-475-16	Sequence 16, App1
2	3080	99.8	609	2	US-09-115-475-28	Sequence 28, App1
3	3080	99.8	609	2	US-09-115-475-31	Sequence 31, App1
4	3079	99.8	609	2	US-09-115-475-25	Sequence 25, App1
5	3071	99.5	609	2	US-09-115-475-19	Sequence 19, App1
6	3066	99.4	609	2	US-09-115-475-22	Sequence 22, App1
7	2876	93.2	651	2	US-09-1489-039A-10691	Sequence 10691, A
8	2510	81.4	622	2	US-09-543-681A-17522	Sequence 7522, App1
9	1919	64.6	616	2	US-09-252-991A-19164	Sequence 19164, A
10	1780	57.7	613	2	US-09-328-352-3066	Sequence 5066, App1
11	1492	48.4	619	2	US-09-540-236-2182	Sequence 2182, App1
12	1362	44.2	572	2	US-09-1902-540-16012	Sequence 16012, A
13	1357	44.0	592	1	US-08-599-171A-30	Sequence 30, App1
14	1357	44.0	592	1	US-08-646-590B-30	Sequence 30, App1
15	1357	44.0	592	2	US-09-069-226-30	Sequence 30, App1
16	1357	44.0	592	2	US-09-412-184-30	Sequence 30, App1
17	1155	37.4	611	2	US-09-438-185A-970	Sequence 970, App1
18	1137	36.8	655	2	US-09-532A-4425	Sequence 4425, App1
19	1117	36.2	602	2	US-09-583-110-4085	Sequence 4085, App1
20	1117	36.2	635	2	US-09-107-433-5022	Sequence 5022, App1
21	1103	36.2	619	2	US-09-134-001C-4248	Sequence 4248, App1
22	1103	35.8	682	1	US-09-911-445-3	Sequence 3, App1
23	1103	35.8	682	2	US-09-182-983-3	Sequence 3, App1
24	1103	35.8	682	2	US-09-771-838A-3	Sequence 6591, App1
25	1103	35.8	680	2	US-09-949-016-0591	Sequence 6, App1
26	1089	35.3	35.3			

ALIGNMENTS

RESULT 1
US-09-115-475-16
; Sequence 16, Application US/09115475
; Patent No. 6372457
; GENERAL INFORMATION:
; APPLICANT: Berry, Alan
; APPLICANT: Burlingame, Richard P.
; APPLICANT: Millis, James R.
; TITLE OF INVENTION: PROCESSES AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE
; FILE REFERENCE: 3161-18-C1
; CURRENT APPLICATION NUMBER: US/09/115,475
; CURRENT FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: PCT/US98/00800
; EARLIER FILING DATE: 1998-01-14
; EARLIER APPLICATION NUMBER: 60/035,494
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-115-475-16

Query Match 100.0%; Score 3086; DB 2; Length 609;
Best Local Similarity 100.0%; Pred. No. 3.7e-295;
Matches 609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCGIVGATAQDVAILEGIRRLERGYYDASGLAVDAGEMTRLRLGKVQMLAQAE 60
Db 1 MCGIVGATAQDVAILEGIRRLERGYYDASGLAVDAGEMTRLRLGKVQMLAQAE 60
QY 1 EPHLHGTTGIAHTRWATHGEPESEVNAHPVSEIIVVVVNGIIENHEPREEELKARYTFV 120
Db 61 EPHLHGTTGIAHTRWATHGEPESEVNAHPVSEIIVVVVNGIIENHEPREEELKARYTFV 120
QY 121 SETDTEVIAHLYNWEILKQGGTLRBAVLRPAIPOLRGAYCTVIMDSRHPDTLAAARGSPLV 180
Db 121 SETDTEVIAHLYNWEILKQGGTLRBAVLRPAIPOLRGAYCTVIMDSRHPDTLAAARGSPLV 180
QY 241 YDAG5DKG1YRHYNQKEIYEQPNIAKNTLGRISHQVQDSELGPNADELLSKVHIIQILA 300
Db 241 YDAG5DKG1YRHYNQKEIYEQPNIAKNTLGRISHQVQDSELGPNADELLSKVHIIQILA 300
QY 301 CGTSYNSGMVSRYWFESLAGIPCDVEIAESBFRYRKAVERRNSLMTLSQSGETADTLAQL 360

RESULT 2
 US-09-115-475-28
 Sequence 28, Application US/09115475
 Patent No. 6372557
 GENERAL INFORMATION:
 APPLICANT: Berry, Alan
 APPLICANT: Burlingame, Richard P.
 ATTORNEY: Millis, James R.
 TITLE OF INVENTION: PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE
 FILE REFERENCE: 316-18-CL
 CURRENT APPLICATION NUMBER: US/09-115,475
 CURRENT FILING DATE: 1998-07-15
 EARLIER APPLICATION NUMBER: PCT/US98/00800
 EARLIER FILING DATE: 1998-01-14
 EARLIER APPLICATION NUMBER: 60/035,494
 EARLIER FILING DATE: 1997-01-14
 NUMBER OF SEQ ID NOS: 31
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 28
 LENGTH: 609
 TYPE: PRT
 ORGANISM: Escherichia coli
 US-09-115-475-28

Query Match 99.8%; Score 3080; DB 2; Length 609;
 Best Local Similarity 99.8%; Pred. No. 1.5e-24;
 Matches 608; Conservative 1; Indels 0; Gaps 0;

Qy 1 MCGIVGAIQRDVAELLEGLRRLERYCGDSAGLAVDAEGMTRRLRGVQMLAQAE 60
 Db 1 MCGIVGALAQRDVAELLEGLRRLERYCGDSAGLAVDAEGMTRRLRGVQMLAQAE 60
 Qy 61 EPHLHGTTGIAHTRWATGEPESEVNAHPVSHIIVHHNGTIEHPLRBELKARGYTFV 120
 Db 61 EPHLHGTTGIAHTRWATGEPESEVNAHPVSHIIVHHNGTIEHPLRBELKARGYTFV 120
 Qy 121 SETDTEVIAHLVNLWELKOGGTIREAVLRAIPLRGAYGTIVMDSRHDPTLAAARSGSPLV 180
 Db 121 SETDTEVIAHLVNLWELKOGGTIREAVLRAIPLRGAYGTIVMDSRHDPTLAAARSGSPLV 180
 Qy 181 IGLGMGENFIASDQLLIPVTRRFILEGDTIAETPRSNIFDKTGAEVKRQDIESNLQ 240
 Db 181 IGLGMGENFIASDQLLIPVTRRFILEGDTIAETPRSNIFDKTGAEVKRQDIESNLQ 240
 Qy 241 YDAGDKG1YRHYNQKEIYQPNIAKNTLGRISHQVDLSELGPNADELLSKVHEHQIILA 300
 Db 241 YDAGDKG1YRHYNQKEIYQPNIAKNTLGRISHQVDLSELGPNADELLSKVHEHQIILA 300
 Qy 301 CGTSYNSGMVSRYWFESLAGIPCDVEIASFRYRKSAVRNSLMTLSQSGETADTLAGL 360

RESULT 3
 US-09-115-475-31
 Sequence 31, Application US/09115475
 Patent No. 6372457
 GENERAL INFORMATION:
 APPLICANT: Berry, Alan
 APPLICANT: Burlingame, Richard P.
 ATTORNEY: Millis, James R.
 TITLE OF INVENTION: PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE
 FILE REFERENCE: 316-1-CL
 CURRENT APPLICATION NUMBER: US/09/115,475
 CURRENT FILING DATE: 1998-07-15
 EARLIER APPLICATION NUMBER: PCT/US98/00800
 EARLIER FILING DATE: 1998-01-14
 EARLIER APPLICATION NUMBER: 60/035,494
 EARLIER FILING DATE: 1997-01-14
 NUMBER OF SEQ ID NOS: 31
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 31
 LENGTH: 609
 TYPE: PRT
 ORGANISM: Escherichia coli
 US-09-115-475-31

Query Match 99.8%; Score 3080; DB 2; Length 609;
 Best Local Similarity 99.8%; Pred. No. 1.5e-24;
 Matches 608; Conservative 1; Indels 0; Gaps 0;

Qy 1 MCGIVGAIQRDVAELLEGLRRLERYCGDSAGLAVDAEGMTRRLRGVQMLAQAE 60
 Db 1 MCGIVGAIQRDVAELLEGLRRLERYCGDSAGLAVDAEGMTRRLRGVQMLAQAE 60
 Qy 61 EPHLHGTTGIAHTRWATGEPESEVNAHPVSHIIVHHNGTIEHPLRBELKARGYTFV 120
 Db 61 EPHLHGTTGIAHTRWATGEPESEVNAHPVSHIIVHHNGTIEHPLRBELKARGYTFV 120
 Qy 121 SETDTEVIAHLVNLWELKOGGTIREAVLRAIPLRGAYGTIVMDSRHDPTLAAARSGSPLV 180
 Db 121 SETDTEVIAHLVNLWELKOGGTIREAVLRAIPLRGAYGTIVMDSRHDPTLAAARSGSPLV 180
 Qy 181 IGLGMGENFIASDQLLIPVTRRFILEGDTIAETPRSNIFDKTGAEVKRQDIESNLQ 240
 Db 181 IGLGMGENFIASDQLLIPVTRRFILEGDTIAETPRSNIFDKTGAEVKRQDIESNLQ 240
 Qy 241 YDAGDKG1YRHYNQKEIYQPNIAKNTLGRISHQVDLSELGPNADELLSKVHEHQIILA 300
 Db 241 YDAGDKG1YRHYNQKEIYQPNIAKNTLGRISHQVDLSELGPNADELLSKVHEHQIILA 300
 Qy 301 CGTSYNSGMVSRYWFESLAGIPCDVEIASFRYRKSAVRNSLMTLSQSGETADTLAGL 360

RESULT 4
US-09-115-475-25
; Sequence 25; Application US/09115475
; Patent No. 6372457
; GENERAL INFORMATION:
; APPLICANT: Berry, Alan
; APPLICANT: Burlingame, Richard P.
; APPLICANT: Millis, James R.
; TITLE OF INVENTION: PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE
; FILE REFERENCE: 3161-18-C1
; CURRENT APPLICATION NUMBER: US/09/115,475
; EARLIER APPLICATION NUMBER: PCT/US98/00800
; EARLIER FILING DATE: 1998-01-14
; EARLIER APPLICATION NUMBER: 60/035,494
; EARLIER FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Escherichia coli
; US-09-115-475-25

Query Match 99.8%; Score 3079; DB 2; Length 609;
Best Local Similarity 99.8%; Pred. No. 1.8e-294;
Matches 608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MCGIVGAIQDVAILELLERLLEYRGDSAGLAVIDDEAGHMTLRRIGKVQMLAQAE 60
Db 1 MCGIVGAIQDVAILELLERLLEYRGDSAGLAVIDDEAGHMTLRRIGKVQMLAQAE 60

Qy 61 EHPLHGTTGTAHTRWAHGEPSEYNAHPHSEHLYVYVINGLILENHEPLREBELKARGYTV 120
Db 61 EHPLHGTTGTAHTRWAHGEPSEYNAHPHSEHLYVYVINGLILENHEPLREBELKARGYTV 120

Qy 121 SETDTEVIAHLVNLKQGTLREAVTRAIPOLRGAYGTIMDSRHPDTLAAARSGPV 180
Db 121 SETDTEVIAHLVNLKQGTLREAVTRAIPOLRGAYGTIMDSRHPDTLAAARSGPV 180

Qy 181 IGLGMGENFIASDQLALLPTTRRFLEEGDIAETTRSVNIFDTGAEVKRDIESNQ 240
Db 181 IGLGMGENFIASDQLALLPTTRRFLEEGDIAETTRSVNIFDTGAEVKRDIESNQ 240

Qy 241 YDAGDKGIVRHYMOKEIYEOPNAIKNTLGRIHSQDVLSELGNADELSKVHBIQILA 300
Db 241 YDAGDKGIVRHYMOKEIYEOPNAIKNTLGRIHSQDVLSELGNADELSKVHBIQILA 300

Qy 301 CGTSGNSGMVSRYMFESLAGIPCDVEIASEFRYRKSAYVRNSLMTLSQSGETADTLAGL 360

Db 301 CGTSGNSGMVSRYMFESLAGIPCDVEIASEFRYRKSAYVRNSLMTLSQSGETADTLAGL 360

Qy 361 RLSKELGYLGSLATACNVPGSSLVRESDLALMTNAGTEIGVASTAFTQTLVLLVAKL 420
Db 361 RLSKELGYLGSLATACNVPGSSLVRESDLALMTNAGTEIGVASTAFTQTLVLLVAKL 420

Qy 421 SRLKGOLDAS1EHDIVGLQALPSREQMSQDR1EALDEDFSDKHHAFLGRODQYPA 480
Db 421 SRLKGOLDAS1EHDIVGLQALPSREQMSQDR1EALDEDFSDKHHAFLGRODQYPA 480

Qy 481 LEGALKLKREISYIHAAYAAGELKGPLALIDAMPVIVAPNNELEKLSNS1BEVRAR 540
Db 481 LEGALKLKREISYIHAAYAAGELKGPLALIDAMPVIVAPNNELEKLSNS1BEVRAR 540

Qy 541 GGOLYVFAQDAGTWSNDMH1IEMPHVEEVIAPIFYTVPLQLLAYHVYALIKGTDVDQPR 600
Db 541 GGOLYVFAQDAGTWSNDMH1IEMPHVEEVIAPIFYTVPLQLLAYHVYALIKGTDVDQPR 600

Qy 601 NLAKSVTVE 609
Db 601 NLAKSVTVE 609

RESULT 5
US-09-115-475-19
; Sequence 19; Application US/09115475
; Patent No. 6372457
; GENERAL INFORMATION:
; APPLICANT: Berry, Alan
; APPLICANT: Burlingame, Richard P.
; APPLICANT: Millis, James R.
; TITLE OF INVENTION: PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE
; FILE REFERENCE: 3161-18-C1
; CURRENT APPLICATION NUMBER: US/09/115,475
; CURRENT FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: PCT/US98/00800
; EARLIER FILING DATE: 1998-01-14
; EARLIER APPLICATION NUMBER: 60/035,494
; EARLIER FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Escherichia coli
; US-09-115-475-19

Query Match 99.5%; Score 3071; DB 2; Length 609;
Best Local Similarity 99.5%; Pred. No. 1.1e-293;
Matches 608; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MCGIVGAIQDVAILELLERLLEYRGDSAGLAVIDDEAGHMTLRRIGKVQMLAQAE 60
Db 1 MCGIVGAIQDVAILELLERLLEYRGDSAGLAVIDDEAGHMTLRRIGKVQMLAQAE 60

Qy 61 EHPLHGTTGTAHTRWAHGEPSEYNAHPHSEHLYVYVINGLILENHEPLREBELKARGYTV 120
Db 61 EHPLHGTTGTAHTRWAHGEPSEYNAHPHSEHLYVYVINGLILENHEPLREBELKARGYTV 120

Qy 121 SETDTEVIAHLVNLKQGTLREAVTRAIPOLRGAYGTIMDSRHPDTLAAARSGPV 180
Db 121 SETDTEVIAHLVNLKQGTLREAVTRAIPOLRGAYGTIMDSRHPDTLAAARSGPV 180

Qy 181 IGLGMGENFIASDQLALLPTTRRFLEEGDIAETTRSVNIFDTGAEVKRDIESNQ 240
Db 181 IGLGMGENFIASDQLALLPTTRRFLEEGDIAETTRSVNIFDTGAEVKRDIESNQ 240

Qy 241 YDAGDKGIVRHYMOKEIYEOPNAIKNTLGRIHSQDVLSELGNADELSKVHBIQILA 300
Db 241 YDAGDKGIVRHYMOKEIYEOPNAIKNTLGRIHSQDVLSELGNADELSKVHBIQILA 300

Qy 301 CGTSGNSGMVSRYMFESLAGIPCDVEIASEFRYRKSAYVRNSLMTLSQSGETADTLAGL 360

RESULT 6
 US-09-115-475-22
 ; Sequence 22, Application US/09115475
 ; Patent No. 6372457
 ; GENERAL INFORMATION:
 ; APPLICANT: Berry, Alan
 ; APPLICANT: Burlingame, Richard P.
 ; APPLICANT: Millis, James R.
 ; TITLE OF INVENTION: PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE
 ; FILE REFERENCE: 3161-18 CL
 ; CURRENT FILING DATE: 1998-07-15
 ; EARLIER APPLICATION NUMBER: PCT/US98/008800
 ; EARLIER FILING DATE: 1998-01-14
 ; EARLIER APPLICATION NUMBER: 60/035, 494
 ; EARLIER FILING DATE: 1997-01-14
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 22
 ; LENGTH: 609
 ; TYPE: PRT
 ; ORGANISM: Escherichia coli
 ; US-09-115-475-22

Query Match 99.4%; Score 3068; DB 2; Length 609;
 Best Local Similarity 99.5%; Pred. No. 2,2e-233; Indels 0; Gaps 0;
 Matches 606; Conservative 3; Mismatches 0;

Qy 1 MCGIVGAIQDYAELLEGLRLLEYRGDSAGLAVDAEGIMTRRLRGKVMLQAEE 60
 Db 1 MCGIVGAIQDYAELLEGLRLLEYRGDSAGLAVDAEGIMTRRLRGKVMLQAEE 60
 Qy 61 EPHLHGTTGIAHTRWATHGEPEVNAHPSEHIVVHNGIENHEPLBELKARGYTFV 120
 Db 61 EPHLHGTTGIAHTRWATHGEPEVNAHPSEHIVVHNGIENHEPLBELKARGYTFV 120
 Qy 121 SETDTEVIAHLVWELKOGTTLREAVRLRAIPOLRGAYTVIMDSRHPDTLAAARSGSPLV 180
 Db 121 SETDTEVIAHLVWELKOGTTLREAVRLRAIPOLRGAYTVIMDSRHPDTLAAARSGSPLV 180
 Qy 181 IGLGMGENFIASDQLALLPVTRRFILEEGDIAETTRRSVNFDTGTAEVKRDIESNLQ 240
 Db 181 IGLGMGENFIASDQLALLPVTRRFILEEGDIAETTRRSVNFDTGTAEVKRDIESNLQ 240
 Qy 241 YDGDKGTYRHYNQKEIYEQPNAAKNTLGRISHQVDSLSEGPNADELLSKVHEHQIILA 300
 Db 241 YDGDKGTYRHYNQKEIYEQPNAAKNTLGRISHQVDSLSEGPNADELLSKVHEHQIILA 300
 Qy 301 CGTSYNSGMVSRWYFESLAGIPCDVETASEPRYRKSAVRNSLMTLSQSGETADTLAGL 360
 Db 301 CGTSYNSGMVSRWYFESLAGIPCDVETASEPRYRKSAVRNSLMTLSQSGETADTLAGL 360

Query Match 93.2%; Score 2876; DB 2; Length 651;
 Best Local Similarity 92.1%; Pred. No. 2,2e-274;
 Matches 561; Conservative 29; Mismatches 19; Indels 0; Gaps 0;

Qy 1 MCGIVGAIQDYAELLEGLRLLEYRGDSAGLAVDAEGIMTRRLRGKVMLQAEE 60
 Db 43 MCGIVGAVAGDIAELLEGLRLLEYRGDSAGLAVDAEGIMTRRLRGKVMLQAEE 102
 Qy 61 EPHLHGTTGIAHTRWATHGEPEVNAHPSEHIVVHNGIENHEPLBELKARGYTFV 120
 Db 103 EPHLHGTTGIAHTRWATHGEPEVNAHPSEHIVVHNGIENHEPLBELKARGYTFV 120
 Qy 121 SETDTEVIAHLVWELKOGTTLREAVRLRAIPOLRGAYTVIMDSRHPDTLAAARSGSPLV 180
 Db 163 TETDTEVIAHLVWELKOGTTLREAVRLRAIPOLRGAYTVIMDSRHPDTLAAARSGSPLV 222
 Qy 181 IGLGMGENFIASDQLALLPVTRRFILEEGDIAETTRRSVNFDTGTAEVKRDIESNLQ 240
 Db 223 IGLGMGENFIASDQLALLPVTRRFILEEGDIAETTRRSVNFDTGTAEVKRDIESNLQ 282
 Qy 241 YDGDKGTYRHYNQKEIYEQPNAAKNTLGRISHQVDSLSEGPNADELLSKVHEHQIILA 300
 Db 283 YDGDKGTYRHYNQKEIYEQPNAAKNTLGRISHQVDSLSEGPNADELLSKVHEHQIILA 342
 Qy 301 CGTSYNSGMVSRWYFESLAGIPCDVETASEPRYRKSAVRNSLMTLSQSGETADTLAGL 360
 Db 343 CGTSYNSGMVSRWYFESLAGIPCDVETASEPRYRKSAVRNSLMTLSQSGETADTLAGL 402
 Qy 361 RLSKELGYLGSLSAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFFTQVLLMLVAKL 420

Query Match 93.2%; Score 2876; DB 2; Length 651;
 Best Local Similarity 92.1%; Pred. No. 2,2e-274;
 Matches 561; Conservative 29; Mismatches 19; Indels 0; Gaps 0;

Qy 1 MCGIVGAIQDYAELLEGLRLLEYRGDSAGLAVDAEGIMTRRLRGKVMLQAEE 60
 Db 43 MCGIVGAVAGDIAELLEGLRLLEYRGDSAGLAVDAEGIMTRRLRGKVMLQAEE 102
 Qy 61 EPHLHGTTGIAHTRWATHGEPEVNAHPSEHIVVHNGIENHEPLBELKARGYTFV 120
 Db 103 EPHLHGTTGIAHTRWATHGEPEVNAHPSEHIVVHNGIENHEPLBELKARGYTFV 120
 Qy 121 SETDTEVIAHLVWELKOGTTLREAVRLRAIPOLRGAYTVIMDSRHPDTLAAARSGSPLV 180
 Db 163 TETDTEVIAHLVWELKOGTTLREAVRLRAIPOLRGAYTVIMDSRHPDTLAAARSGSPLV 222
 Qy 181 IGLGMGENFIASDQLALLPVTRRFILEEGDIAETTRRSVNFDTGTAEVKRDIESNLQ 240
 Db 223 IGLGMGENFIASDQLALLPVTRRFILEEGDIAETTRRSVNFDTGTAEVKRDIESNLQ 282
 Qy 241 YDGDKGTYRHYNQKEIYEQPNAAKNTLGRISHQVDSLSEGPNADELLSKVHEHQIILA 300
 Db 283 YDGDKGTYRHYNQKEIYEQPNAAKNTLGRISHQVDSLSEGPNADELLSKVHEHQIILA 342
 Qy 301 CGTSYNSGMVSRWYFESLAGIPCDVETASEPRYRKSAVRNSLMTLSQSGETADTLAGL 360
 Db 343 CGTSYNSGMVSRWYFESLAGIPCDVETASEPRYRKSAVRNSLMTLSQSGETADTLAGL 402
 Qy 361 RLSKELGYLGSLSAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFFTQVLLMLVAKL 420

Db 403 RLSKELGYJSLAICNPGSSLVRESDALMTRKAGE1GVASTKRAFTQJLTVLMLVAK 462
 Qy 421 SRLKLDAS1EHD1VHGLQALPSREQMSQDKRIEALDEDPSDKHHALFGLGCDQYPA 480
 Db 463 ARLKQDAS1EHD1VHGLQALPNEQMSQDKRIEOLERFSDKHHALFGLGCDQYPA 522
 Qy 481 LEGALKLKKEISYHAEAYAEGELKGPLLALIDAMPVIVAPNNELEKLSNS1EEVRA 540
 Db 523 MEGALKLKKEISYHAEAYAEGELKGPLLALIDAMPVIVAPNNELEKLSNS1EEVRA 582
 Qy 541 GGOLYVFAODAGTVSSDMH1EMPHVEVIAPIPYTPLQLAYHVALIKGTDVDQPR 600
 Db 554 GGOLYVFAODAGFEESETMKL1SLPVHVEELIAP1FYTPLQLISYHVALIKGTDVDQPR 613
 Qy 601 NLAKSVTVE 609
 Db 614 NLAKSVTVE 622

RESULT 9
 US-09-252-991A-19164
 ; Sequence 19164, Application US/09252991A
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196_136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIORITY APPLICATION NUMBER: US 60/074,788
 ; PRIORITY FILING DATE: 1998-02-18
 ; PRIORITY APPLICATION NUMBER: US 60/094,190
 ; PRIORITY FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO: 19164
 ; LENGTH: 616
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-19164

Query Match 64.6%; Score 1995; DB 2; Length 616;
 Best Local Similarity 62.7%; Pred. No. 1 7e-187;
 Matches 363; Conservative 101; Mismatches 125; Indels 2; Gaps 2;

Db 1 MCGIVGAAORDVABILLEGRLRLEYRGYDSAGLAVVDAEGHMTLRLRGKYMIAQAAE 60
 Qy 1 MCGIVGAAORDVABILLEGRLRLEYRGYDSAGLAVVDAEGHMTLRLRGKYMIAQAAE 60
 Db 6 MCGIVGAAORDVABILLEGRLRLEYRGYDSAGVFDNEGRLQRCCRQGVASLEEGLA 65
 Qy 1 MCGIVGAAORDVABILLEGRLRLEYRGYDSAGLAVVDAEGHMTLRLRGKYMIAQAAE 60
 Db 11 EHPLHGGCTGAHTTWATHGEPESEYNAHPHV-SEHIVVHNG1LENHEPLREELKARGYTF 119
 Qy 66 GTPPLGRGLGTAHTTWATHGAPTEENAHPHFSSDELAHVHNG1LENHEPLREELKGLGYVF 125
 Db 120 VSETDTEVIAHLYNWLKGQTTRAEAVRA1PQLRAYGTIVMDSRHPDTLLAARSGPL 179
 Qy 126 TSQDTDETVHLLHKLQSIGDTLTAKDKEIHLGAGLAVISAQOPRIVARSGPL 185
 Db 180 VIGLGMGENFIASDQAL1LPVTRF1FLEGGDIAETTRSVN1FDKTGAEVKRODIESNL 239
 Qy 186 VIGLGMGENFIASDQAL1LPVTRF1FLEGGDIAETTRSVN1FDKTGAEVKRODIESNL 239
 Db 240 QYDQDGKGTYRHYMQKEIYEQPNALKNTLGRISHQVDSLGPNADELSKVHEHQ1L 299
 Qy 246 GAEADKGBYRFHMLKEIHEQPSVYQRTLEGRLQCNQWVSECPQAAELFAKTRVQIV 305
 Db 300 AGCTSYNSGRVSYRFESLQFEDVETASEFRYRKSAVRNLS1ITLQSGETADTLAG 359
 Db 306 AGCTSYHAGMVAWTWLESLTGIPQCVEASEFRYRKAVQPDCLFLVFT1QSGETADTLAA 365
 Db 360 LRLSKELGYGLS1AICNPGSSLVRESDALMTRKAGE1GVASTKRAFTQJLTVLMLVAK 419
 Qy 366 LRNKEALGPFSVAAICNVTSSLVRRESDTLTOAQP1GVASTKRAFTQJLTVLMLVAK 425
 Db 420 LSRL-KGLDAS1EHD1VHGLQALPSREQMSQDKRIEALAEFSKXHHALFGLGCDQYD 478
 Qy 426 IGQVQKRLADGVAEALVDELRRLPTRLGEALANRTRVKESELPEKHTFLGRGAQPP 485

RESULT 8
 US-09-543-681A-7522
 ; Sequence 7522, Application US/09543681A
 ; Patent No. 6605709
 ; GENERAL INFORMATION:
 ; APPLICANT: NANCY BRETON
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
 ; FILE REFERENCE: 2709.1002-001
 ; CURRENT APPLICATION NUMBER: US/09/543,681A
 ; CURRENT FILING DATE: 2000-04-05
 ; PRIORITY APPLICATION NUMBER: US 60/128,706
 ; PRIORITY FILING DATE: 1999-04-09
 ; NUMBER OF SEQ ID NOS: 8344
 ; SEQ ID NO: 7522
 ; LENGTH: 622
 ; TYPE: PRT
 ; ORGANISM: Proteus mirabilis
 US-09-543-681A-7522

Query Match 81.4%; Score 2510.5; DB 2; Length 622;
 Best Local Similarity 81.1%; Pred. No. 2.4e-238;
 Matches 494; Conservative 46; Mismatches 68; Indels 1; Gaps 1;

Qy 1 MCGIVGAAORDVABILLEGRLRLEYRGYDSAGLAVVDAEGHMTLRLRGKYMIAQAAE 60
 Db 15 MCGIVGAAORDVABILLEGRLRLEYRGYDSAGLAVVDAEGHMTLRLRGKYMIAQAAE 74
 Qy 61 EHPLHGGCTGAHTTWATHGEPESEYNAHPHV-SEHIVVHNG1LENHEPLREELKARGYTF 120
 Db 75 KTOVGGTGAHTTWATHGAPTEENAHPHFSSDELAHVHNG1LENHEPLREELKGLGYVF 134
 Qy 121 SETDTEVIAHLYNWLKGQTTRAEAVRA1PQLRAYGTIVMDSRHPDTLLAARSGPL 180
 Db 135 SQTDEVIAHLYNWLKGQTTRAEAVRA1PQLRAYGTIVMDSRHPDTLLAARSGPL 194
 Qy 181 IGLGMGENFIASDQAL1LPVTRF1FLEGGDIAETTRSVN1FDKTGAEVKRODIESNL 240
 Db 195 VGLGYGENFIASDQAL1LPVTRF1FLEGGDIAETTRSVN1FDKTGAEVKRODIESNL 254
 Qy 241 YDAGDKGITYRHYMQKEIYEQPNALKNTLGRISHQVDSLGPNADELSKVHEHQ1L 300
 Db 255 YDAGDKGITYRHYMQKEIYEQPNALKNTLGRISHQVDSLGPNADELSKVHEHQ1L 314
 Qy 301 CGTTSNNSGAVSYRWFESLQFAGIPCDV1ASFRYKSAVRNLS1ITLQSGETADTLAG 360
 Db 315 CGTTSNAGMYSRWFESLQFAGIPCDV1ASFRYKPAVRNLS1ITLQSGETADTLAG 374
 Qy 361 RLSKELGYGLS1AICNPGSSLVRESDALMTRKAGE1GVASTKRAFTQJLTVLMLVAK 420
 Db 375 RLSKELGYGLS1AICNPGSSLVRESDALMTRKAGE1GVASTKRAFTQJLTVLMLVAK 434
 Qy 422 SRLKLDAS1EHD1VHGLQALPSREQMSQDKRIEALAEFSKXHHALFGLGCDQYPA 480

Qy 479 TALEGALKLKEISYTHAAAYAAGELKHGPALIADMPVIVVAPNNELEKLSNIREVR 538
 Db 486 VALBALKIKLEISYTHAAAYAAGELKHGPALIADMPVIVVAPNNELEKLSNIREVR 545
 Qy 539 ARGGOLYVFAODQAFVSSDNMHITEMPHVEEVIAPIFTYVPLQLLAVHVALIKGTDYDQ 598
 Db 546 ARGGELVVADEGAGIEAGBGTTHVGMPHIGDVLSPILYTIPLQLLSVTHAVLKGTDYDQ 605
 RESULT 11
 US-09-328-352-5066
 Sequence 5066, Application US/09328352
 Patent No. 6562958
 GENERAL INFORMATION:
 APPLICANT: Gary L. Breton et al.
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO ACTINETOBACTER
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO ACTINETOBACTER
 FILE REFERENCE: GTC9-03PA
 CURRENT APPLICATION NUMBER: US/09/328, 352
 CURRENT FILING DATE: 1999-06-04
 SEQ ID NO: 5066
 LENGTH: 613
 TYPE: PRT
 ORGANISM: Acinetobacter baumannii
 US-09-328-352-5066

Query Match 57.7%; Score 1780.5; DB 2; Length 613;
 Best Local Similarity 57.4%; Pred. No. 2.5e-166; Indels 9; Gaps 5;
 Matches 353; Conservative 107; Mismatches 146;

Qy 1 MCGIVGAIARQDYAELIIFGLRLEYGYDSAGLAVYDAEGHMTLRLRGKVQMLAQAA 60
 Db 2 MCGIVGGYAVERCYTEILIGKLRLKLEYRDXSAGVALINKQ-OILRERFVGVINLEPAV 60
 Qy 61 EPHLHGGCTIAHTPWATHEPSEVNAHPVSEHIVVYHNGIENHEPLREELKARGYTFV 120
 Db 61 DQQTGTGIGIAHTPWATHGKPTENNAHPMSGKVAVYHNGIENYQELKDIQALGYVF 120
 Qy 121 SETDTEVIAHLVNLKOCGTLREAVLRAIPLRGAYGTIVMDSRHPDITLAAARGSPV 180
 Db 121 SQIDTEVVAHLVNLKNTDSLBEAVESVPUQKGAVALGIHSYDPLDLTVRESPV 180
 Qy 181 IGLGMGENITASDQLLIPVTRPFLFEGDIBITRSVNIFDKTGAEVKRDIESNLQ 240
 Db 181.1 IGVIGENITISSDQLLIPVTRPFLFEGDIBARLTTSVFK-GERVERPVKELDAT 239
 Qy 241 YDAGDKGYRHYMOKEIYEQPNAKNTLGRISHQVDLSELGPNADELLSKVBTQI 300
 Db 240 VSSASKGEKHYMLKEIYEQPEAKIKOTISQALD-GNNLRRDDFLKDAEADFSKQLOSOVII 298
 Qy 301 CGTTSYNSGVSR/TWESLAGIPCDVIAESEFRYRSKAVRNSLMITUSQSGTADTLAGL 360
 Db 299 CGTTSYHSGMAYKWEQFLQGPQVEADEFRYSRSPVIENTLYCISQSGTADTLA 358
 Qy 361 RLSKELGY ---LGSIAICNYPGSSLYRESDLALMTNAGTRIGVASTKAFTTOLTVLM 415
 Db 359 RETOKRAKANNIDQTLTCAVATSSMVRRETDLHLLTAGPEGVASTKAFTTOLALML 418
 Qy 416 LVAKLSRLKGLDASIE-HDIVHGLQALPSRIEQLMSQDKR1EALAEFSDKXHALFLGRG 474
 Db 419 LILKIGQYKQRIISNMVMEELRLWHSKPLVTLTQKDAEILRLSELFVQHCLFLGRG 478
 Qy 475 DQVPIALEGALKLKEISYTHAAAYAAGELKHGPALIADMPVIVVAPNNELEKLSN 534
 Db 479 THYPIALEGALKLKEISYTHAAAYAAGELKHGPALIADMPVIVVAPNNELEKLSN 538
 Qy 535 EBYRARGQQLYVFAODQAFVSSDNMHIEMPHVEEVIAPIFTYVPLQLLAVHVALIKG 594

Db 539 BEVQARCGELPFVFADENSGVYKDRQHVQTPAVNEWLAPIYSVWVQDLISYHVAFLRG 598
 Qy 595 DVDPQRNLAKSVTVE 609
 Db 599 DVDPQRNLAKSVTVE 613
 RESULT 12
 US-09-540-236-2182
 Sequence 2182, Application US/09540236
 Patent No. 6573910
 GENERAL INFORMATION:
 APPLICANT: Gary L. Breton et al.
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAF
 TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 2709-2005-001
 CURRENT APPLICATION NUMBER: US/09/540, 236
 CURRENT FILING DATE: 2000-04-04
 SEQ ID NO: 2182
 LENGTH: 619
 TYPE: PRT
 ORGANISM: M. catarrhalis
 US-09-540-236-2182

Query Match 48.4%; Score 1492.5; DB 2; Length 619;
 Best Local Similarity 50.3%; Pred. No. 6.8e-138;
 Matches 309; Conservative 112; Mismatches 186; Indels 18; Gaps 7;

Qy 1 MCGIVGAI-AORDVARILLEGLRLRLEYGYDSAGLAVYDAEGHMTLRLRGKVQMLAQAA 59
 Db 8 MCGIVGAAIRTHHNVYFLTDKLRQYRGRGDSQSL-VQYESGTRVRRVGRVALMEEA 66
 Qy 60 BEHPLUGGTGIAHTPWATHEPSEVNAHPVSEHIV-VVNGIENHEPLREELKARGYTF 118
 Db 67 KQKQITQGLTGTGHTKWAHGTVTKNAPHPISAGLJISUWNGIENFETRTRLQHLDYE 126
 Qy 119 FVSETTEVIAHLVNLKOCGTLREAVLRAIPLRGAYGTIVMDSRHPDITLAAARGSPV 177
 Db 127 FESQTEVIAHSVREYTTNGDLYHAVOTACSRFHGAIAVIAVANDAPNQMTARMGC 186
 Qy 178 PLVIGLGMGENFIASDQLLIPVTRFIFEGDIAETTRSV-NIFDKTGAEVKRDIE 236
 Db 187 PLLVARGDNEVYFASVPSVSAVAFTERVTVLTDQDQIQKQLKDQGNOVNRSIKT 246
 Qy 237 SNLQYDAGDKGYRHYMOKEIYEQPNAKNTLGRISHQVDLSELGPNADELLSKVBTQI 296
 Db 247 SEMSLASLLEGPYSHFMQKEINEQPRAVSDTAEFLLEGGVY-ADNFGEEAPEIFAKIQSI 305
 Qy 297 QILACGTTSNNSGMVSRYWFESLAGIPCDVIAESEFRYRSKAVRNSLMTUSQSGTADT 356
 Db 306 KILACGTTSYAAHTLGKHYLESIAKRCDEIAESTKRAFTTOLTVLML 416
 Qy 357 LAGLRLSKELGYLGSIAICNYPGSSLYRESDLALMTNAGTRIGVASTKAFTTOLTVLML 425
 Db 366 MBALKYAMAQHRYSSICNYMEASALPRTSLAIFTRAGEIGVASTKAFTTOLTVLFLGL 425
 Qy 417 VAKLSRLKLGK-LDASIEHDIVHGLQALPSRIEQLMSQDKR1EALAEFSDKXHALFLGRG 475
 Db 426 AVTLGILRGHYDEQADYVAEFLRULPGSQHALNLNEPOLASWAQSFANKPSAFLGRGI 485
 Qy 476 QYPIALEGALKLKEISYTHAAAYAAGELKHGPALIADMPVIVVAPNNELEKLSN 535
 Db 486 HYPIALEGALKLKEISYTHAAAYAAGELKHGPALIADMPVIVVAPNNELEKLSN 545
 Qy 536 EVRARGQOLYVFAODQAFVSSDNMHIEMPHVEEVIAPIFTYVPLQLLAVHVALIKG 595
 Db 546 EVSARGELEVLSLSDYTAESEGVHIIPTPRHGTLSPIVHTIPQVLLAYHVALIKGTD 605
 Qy 596 VDQPRNLAKSVTVE 609
 Db 606 VDKPRNLAKSVTVE 619

RESULT 12

US-09-902-540-16012

Sequence 16012, Application US/0902540

Patent No. 6833447

GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: *Myxococcus xanthus* Genome Sequences and Uses Thereof

FILE REFERENCE: 38-10115849 B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 16012

LENGTH: 572

TYPE: PRT

ORGANISM: *Myxococcus xanthus*

US-09-902-540-16012

Query Match 44.2%; Score 1362.5; DB 2; Length 572;

Best Local Similarity 50.0%; Prod. No. 4e-125; Mismatches 105; Indels 13; Gaps 7;

Matches 279; Conservative 105; Mismatches 161; Indels 13; Gaps 7;

Qy 59 AEEHPLHGGTGIATHRWAHTGPESEVNNAHPHYSBHIVVVHNGLIENHPREPLKARYT 118

Db 21 ADQPP--GNIGIGHTRWAHTGRSDENHPTKDVAVTHNGIENHLSKEQLRSRGH 78

Qy 119 FVSEBTDTTEVIAHLVNWELKQGGTIREAATRAIPOLRGAYGTIMDSRHPDTLLAARSGP 178

Db 79 FSESETDSEPAFHLSBELLGLPDAVRAIAQVKGTYALAVLTASDPSRIVCTDAS 138

Qy 179 LVTIGLGMGENFTASDQLALLPVTRRFITLEEGDIAETTRSYNIFDKTGAEVKRODIESN 238

Db 139 MVTGLGQCNFLASDVPALLEHTRDFTYMEEGDIAVATAAVIDFNGQKVNRPTRID 198

Qy 239 LQYDAGDKGIYRHMOREKLYQPNIAKNTLTGR--ISHGQDLSLEGPNADELLSKYEH 296

Db 199 WTPMMAEKGHKHMHKEWQRAVADTLRGRMLLSEGDVHFGMNLSAEKVRS-LTK 257

Qy 297 QILAGTGSYNSGMVSRYTMPESSLAGIPCDVEIASEFRYKSAVRRNSLMTLSQSGETADT 356

Db 258 TILAGTGSWHSYGAKHMTESLRPVVELEASEFRYRDPIDVGTIIAIAQSQSGETADT 317

Qy 357 LAGLRLSKELGYLGSLAICNVPGSSLYRESDLALMTNAGTEIVGAVASTKAFTQLTIVML 416

Db 318 LAFKEAARG-ATAMACNVCSAMTREADFVLTNAGPEIGVASTKAFTQLTIVML 376

Qy 417 VAKLRLKG--LDASLEH DIVVGLQALPSRLEQMLSDKRIBALAEDPSDKHAFPLGR 473

Db 377 AVKLGRMREGTLSPSAQBEEH-LTQLTKVPMIEDVLKCEPAVTRSVREYMSQDFLGR 434

Qy 474 GDOYPIALLEGALKLKEISYTHAAYAAGELKHGQPLALIDADMIVVYAPN--NELLKLK 531

Db 435 GPMHPVALEGALKLKEISYTHAAGYAGBEMKHGQPLALIDEMHFWVVTAPQPHVATEKI 494

Qy 532 SNTEEVRAARGGOLYVFAAQDAGFVSSDNMTHIEMPHYEEVIAPIFYTVPLQLLAYHVAL 591

Db 495 GNTEEVRAARGGKVTAIDDEDDERIVATLQDQVRIPIAACLLAPVAVTIPQLLAYHVAL 554

Qy 592 KGTDVDQDPNPLAKSVTVE 609

Db 555 RGNDDVDQDPNPLAKSVTVE 572

RESULT 13

US-08-599-171A-30

Sequence 30, Application US/08599171A

Patent No. 5814473

GENERAL INFORMATION:

APPLICANT: Warren, Patrick V.

TITLE: TRANSAMINASES AND AMINOTRANSFERASES

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, STEWART & OLSTEIN

STREET: 6 BECKER FARM ROAD

CITY: ROSELAND

STATE: NEW JERSEY

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH DISKETTE

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/599,171A

FILING DATE: Concurrently

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT & INFORMATION:

NAME: HERRON, CHARLES J.

REGISTRATION NUMBER: 28,019

REFERENCE/DOCKET NUMBER: 331400-38

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 592 AMINO ACIDS

TYPE: AMINO ACID

TOPOLOGY: LINEAR

MOLECULE TYPE: PROTEIN

US-08-599-171A-30

Query Match 44.0%; Score 1357.5; DB 1; Length 592;

Best Local Similarity 46.5%; Prod. No. 1.3e-124;

Matches 286; Conservative 113; Mismatches 187; Indels 29; Gaps 9;

Qy 1 MCGIVGATAQDVA-EILLEGRRLRERGYDASGLAVVDAEGHMTLRLRGKVQMLACAA 59

Db 1 MCGIVGATVGTG-RDIALPVLGALERLERGYDASGVALLE-DGLLIVKEKKKGKIRELYVAL 58

Qy 60 EHPLHPLGSGTGTIAHTRWATHGEPESEVNNAHPHYS-E-HIVVYNGLIEENHEPLREELKARYG 117

Db 59 WGRDYKARTGQHTRWATHGKEDENAHPTDBKGFAVVGVYENYLELKEBLKEGV 118

Qy 118 TFSSETDTEVIAHLVNWELKQGGTIREAATRAIPOLRGAYGTIMDSRHPDTLLAARSGS 177

Db 119 KERSETDTEVIAHLIAKNYR-GDLLEAVLTVKUKLKGAFAPAVITVHEPNRLGIVKROGS 176

Qy 178 PLVIGLGMGENFTASDQLALLPVTRRFITLEEGDIAETTRSYNIFDKTGAEVKRODIESN 237

Db 177 PLVIGLGEGENFLASDPAILPVYTKIVLDGEIAUDTPDVNAYFEGEPVSKEMVIT 236

Qy 238 NIQYDAGDKGIYRHMOREKLYQPNIAKNTLTGRISHGQDLSLEGPNADELL--LSKVE 294

Db 237 PWDLVAEKGHKHMFKEIYQPKAANDTQFLS-----TEDAIPFKLQDFR 285

Qy 295 HIQILACGSTNSGMWSRYWPFSSLAGIPCDVEIASEFRYKSAVRRNSLMTLSQSGETA 354

Db 286 RVLIIACGSTHAGFVKWYIERTFVGTIVYASERVADPVSQDIVGIGISQSGETA 345

Qy 355 DTLAGIQLSKELGYLGSLAICNVPGSSLYRESDLALMTNAGTEIVGAVASTKAFTQLTIVML 414

Db 346 DTKPALOSAKEGAF-TVGLNVVGSAIDRESDFSLTHAEGVAAATKTFTAQFTALY 404

Qy 415 MLVAKLRSRLKGLDASIEHDIVHGLQALPSRTEQMLSQDKRIBAELAEDFSDKHHALFLGRG 474

405 ALSVR-----ESERENLIRLEKPVSLVEQTINTAEEVKAEMKOMMLYGRY 457
 475 DQYPIALEGALKLKEISYIHAAYAEGELKHGPALIDADMPVIVAPNELLKEKLSNI 534
 458 LNYPIALEGALKLKEISYIHAEGYPAGEMKHGPALIDEMMPVIVAPDRVTEKILSNV 517
 535 BEVRARGCQLYVFADQDAGFVSSDMHILEMPHVEETAPIFYVPLOLAYHVALIKGT 594
 518 BEVLARKGRYISVGPKGDETUKSKSESVMEIPKAEPITPFLTVIPLQLOFATIASKLGL 577
 595 DVDPQRNLAKSVTVE 609
 578 DVDPQRNLAKTVTVE 592

RES 14
 US-08-646-590B-30
 ; Sequence 30, Application US/08646590B
 ; GENERAL INFORMATION:
 ; APPLICANT: Warren, Patrick V.
 ; APPLICANT: Swanson, Ronald V.
 ; TITLE OF INVENTION: TRANSMINASES AND AMINOTRANSFERASES
 ; NUMBER OF SEQUENCES: 42
 ; ADDRESSSEE: Fish & Richardson, P.C.
 ; STREET: 4225 Executive Square, Suite 1400
 ; CITY: La Jolla
 ; STATE: CA
 ; COUNTRY: US
 ; ZIP: 92037
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows 95
 ; SOFTWARE: PasteEQ For Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/646,590B
 ; FILING DATE: 08-May-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/599,171
 ; FILING DATE: 09-FEB-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US97/01094
 ; FILING DATE: 21-January-1997
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Haile, Ph.D., Lisa A.
 ; REGISTRATION NUMBER: 09010/017001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619/678-5070
 ; TELEFAX: 619/678-5059
 ; INFORMATION FOR SEQ ID NO: 30:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 592 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: Protein
 ; FRAGMENT TYPE: Internal

US-08-646-590B-30
 Query Match 1: MCGIVGAAQRDVA-EILLEGLRRLERYGDSAGLAVDAEACHMTRLRLSKVQMLAQAA 59
 Best Local Similarity 44.0%; Score 1357.5; DB 1; Length 592;
 Matches 286; Conservative 113; Mismatches 187; Indels 29; Gaps 9;

Db 59 WGKDYKAKTGIGHTRATHGKPTDEAHAPHTDEKGEPFVNGTIEENYLEKEELKKEGV 118
 Qy 118 TFESETDTEVIAHLYWNLKGCGTLEAVERLRAIPOLRGAYGTIVMMSRHPDTLALARSGS 177
 Db 119 KERSETDTEVIAHLYAKNVR-GDLIBAVLKVKKKGAFAPAVTVHEPRLIGRKQGS 176
 Qy 178 PLVIGHGMGENFIASDQALALPVTRFPLFEGDIAEITRRSVNTIDKTKGAEVKRDIES 237
 Db 177 PLVIGLGEGENFLASIDPAPLYTKHIVLVLGDETAIDLTPDTVNTNFEGEPVSKVMIT 236
 Qy 238 NLQYDAGDKGYRHYNQKEIEQPNKIQNTLGRISHGQVDLSELQPNADL--LSKVE 294
 Db 237 PWDLVAEKGFKHMKEYEQPKAINDTLKGFLS-----TEAIPFKLKDKFR 285
 Qy 295 HQQILAGGTNSGMWSRYWFEPSLAGIPCDVIAESFRYRKSAYVRNSLMTLSQSGETA 354
 Db 286 RVLIILAGCTSYTHAGFQKYWIERPAGVPTEVYASERFRAVDPVSDKDIVGQSGETA 345
 Qy 355 DTLAGLRLSKLKGYLQSLAICNVPGSSVLRESIDALMTNAGTEIGVASTKAFTTOLTVLL 414
 Db 346 DTKFALQSAEKGAF-TVGLNVNSAIDESDFSHHTHAGPEIGVAAKTFTAQFTALY 404
 Qy 415 MLVAKLRSRKGLDASLEHDIVHGLQALPSRLEQMSQDKRLEALADFSDKHHALFLGRG 474
 Db 405 ALSVR-----ESERENLIRLLEKRVPSLVEQTUNTAEEVKVAKYMKCKNMLYLGRY 457
 Qy 475 DQYPIALEGALKLKEISYIHAAYAEGELKHGPALIDAMPVIVAPNBNLLEKUSNI 534
 Db 458 LNYPIALEGALKLKEISYIHAEGYPAGEMGHGPALIDENMPVIVAKDRVYEKLSNV 517
 Qy 535 BEVRARGGOLYVFADQDAGFVSSDNMHHIEMPHVEIAPIFTYPTPLQLYAHVALIKGT 594
 Db 518 BEVLARKGRVISVGFGDETUKSKSESVMEIPKAEPITPFLTVIPLQLPAYFIASKLGL 577
 Qy 595 DVDPQRNLAKSVTVE 609
 Db 578 DVDPQRNLAKTVTVE 592

RESULT 15
 US-09-069-226-30
 ; Sequence 30, Application US/09069226
 ; Patent No. 6013509
 ; GENERAL INFORMATION:
 ; APPLICANT: WARREN, Patrick V.
 ; TITLE OF INVENTION: TRANSMINASES AND AMINOTRANSFERASES
 ; NUMBER OF SEQUENCES: 32
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
 ; ADDRESS: 6 BECKER FARM ROAD
 ; STREET: 6 BECKER FARM ROAD
 ; CITY: ROSELAND
 ; STATE: NEW JERSEY
 ; COUNTRY: USA
 ; ZIP: 07068
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 INCH DISKETTE
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: MS-DOS
 ; SOFTWARE: WORD PERFECT 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/069-226
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/599,171
 ; FILING DATE: 09-FEB-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: HERRON, CHARLES J.
 ; REGISTRATION NUMBER: 331400-38
 ; REFERENCE/DOCKET NUMBER: 331400-38
 ; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-994-1700
 ; TELEFAX: 201-994-1744
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 592 AMINO ACIDS
 ; TYPE: AMINO ACID
 ; TOPOLOGY: LINEAR
 ; MOLECULE TYPE: PROTEIN
 us-09-059-226-30

Query Match Score 1357.5; DB 2; Length 592;
 Best Local Similarity 44.0%; Pred. No. 1.3e-124;
 Matches 266; Conservative 113; Mismatches 187; Indels 29; Gaps 9;
 Matches 266; Conservative 113; Mismatches 187; Indels 29; Gaps 9;

Qy 1 MCGIVGAIACORDVA-EILIGLRLRLREYRGYDSDAGLAVVDAEGHNTTRLRGKVQMLAQ 59
 Db 1 MCGIVGIVG-RDLALPIVGALERLEYRGYDSDAGVAVLIE-DGKLVKEKKGKRELVAL 58

Qy 60 EEHPLHGGTGTIAHTRWATHEGPSEVNAHPPHSE--HIVVVFHNGTILENHEPLREELKARGY 117
 Db 59 WGDYKAKTCGKIGHTRWATHEGPSEVNAHPPHSE--HIVVVFHNGTILENHEPLREELKARGV 118

Qy 118 TFSSETDTTEVIAHLYNWEIQLGGTIREAULRAIPLQLRGYGTIVMDSHRPDTLIAARGG 177
 Db 119 KFRSETDTTEVIAHLYAKNTR-GDILEAVLKTVKLKGFAFAVITVHEPNRLJIGVKQGS 176

Qy 178 PLVIGLMGENFIASDOLLALLPVTTRFIFLEEGDIAETTRSYNIFDKTGAEVYKRODIES 237
 Db 177 PLVIGLGEGENFLASDIPAILPTYKIIIVDDGEADLPPDTWVNFEGEPVSKEMVIT 236

Qy 238 NLQYDAGDKGIVYRHYMOKELYEQPNAIKNTLGRISHGGQVDLSELGPNADEL--LSKVE 294
 Db 237 PWDLVAEBCGGFKEFMLKEYEQPNAIKNTLKGFLS-----TEDAIPFKLKDFR 285

Qy 295 HIQIACGTSYNSGMVSRNTWESLAGIPCDPELASEFRTKSAYVRNSLIMITSQSGETA 354
 Db 286 RVLIIACGTSYHAGFVGKWIERRAGVPPVIVASEFRTADVPVPSDKIVIGISQSGETA 345

Qy 355 DTLAQLRLSRELGYLGSIAICNPYGSLLYRESIDLALMTNAGTEIGVASTKRAFTQLTVL 414
 Db 346 DTKPALQSKEKGAF-TVGLVNVVGSATRDESDFSLTHAGPEIGVAATKTPAQFTALY 404

Qy 415 MLVAKLSSLRKLGLDASIEHDIVHGLAOALPSRTEQMLSDOKRIEALAEFDGKHALFLGRG 474
 Db 405 ALSTR-----EEBERENLRLKEVKLIVQELVOTLNTAEVEKVKYKMKMLYLGRY 457

Qy 475 DQYPALEGALKLKEISIHAAYAAGLLEHGPALIADMPVIVAPNNEELJKLKSNI 534
 Db 458 LNYPFALEGALKLKEISIHAEGPAGEMKHGPALIDENMPVIVIAKDRVYEBKILSN 517

Qy 535 EEPVARGGOLYVFADQDAGFVSSDNMHILEMPHVEEVIAPIFYTVPLOLLAYHVALIKGT 594
 Db 518 BEVLARKGRTISVGPKGDETLKSSESVNEIPKAEPITPFLTVIPLQLPAYFTASKGL 577

Qy 595 DVQPRNLAKSVTVE 609
 Db 578 DVQPRNLAKTVVE 592

Result No.	Score	Query Match	Length	DB ID	Description
1	3086	100.0	609	3	US-09-815-242-10399 Sequence 10399, A
2	3086	100.0	609	4	US-10-024-460-16 Sequence 16, Appl
3	3086	100.0	609	4	US-10-369-493-23611 Sequence 23611, A
4	3086	100.0	609	4	US-10-282-122A-56753 Sequence 56753, A
5	3086	100.0	609	4	US-10-612-779-2 Sequence 2, Appl
6	3086	100.0	609	5	US-10-823-397-23 Sequence 23, Appl
7	3080	99.8	609	4	US-10-024-460-28 Sequence 28, Appl
8	3080	99.8	609	4	US-10-024-460-31 Sequence 31, Appl
9	3080	99.8	609	4	US-10-612-779-10 Sequence 10, Appl
10	3080	99.8	609	4	US-10-612-779-12 Sequence 12, Appl
11	3079	99.8	609	4	US-10-024-460-25 Sequence 25, Appl
12	3079	99.8	609	4	US-10-612-779-8 Sequence 8, Appl
13	3071	99.5	609	4	US-10-024-460-19 Sequence 19, Appl
14	3071	99.5	609	4	US-10-612-779-4 Sequence 4, Appl
15	3068	99.4	609	4	US-10-024-460-22 Sequence 22, Appl
16	3068	99.4	609	4	US-10-612-779-6 Sequence 6, Appl
17	3068	99.4	609	5	US-10-823-397-25 Sequence 25, Appl
18	3061	99.2	609	4	US-10-612-779-14 Sequence 14, Appl
19	3053	98.9	609	3	US-09-815-242-14065 Sequence 14065, A
20	3053	98.9	609	4	US-10-282-122A-76152 Sequence 76152, A
21	2950	95.6	609	4	US-10-282-122A-56279 Sequence 56279, A
22	2876	93.2	609	3	US-09-815-242-11758 Sequence 11758, A
23	2871	93.0	609	4	US-10-282-122A-59335 Sequence 59335, A
24	2718	88.1	608	4	US-10-282-122A-72965 Sequence 72965, A
25	2682	86.9	609	4	US-10-282-122A-78533 Sequence 78533, A
26	2661	86.2	609	4	US-10-369-493-21242 Sequence 21242, A
27	2619	84.9	609	4	US-10-369-493-438 Sequence 438, App

Db	61 EPLHGGTGIATRWAHGEPESEVNAHPVSEHIVVINGIENHEPLREELKARGYTFV 120	Db	61 EHPLHGGTGIATRWAHGEPESEVNAHPVSEHIVVHNGIENHEPLREELKARGYTFV 120
Qy	121 SETDDEVIAHLVNWLKGCGTIREAVLAIPOLRGAYGTVIMDSRHPDTLLAARSGLV 180	Qy	121 SETDDEVIAHLVNWLKGCGTIREAVLAIPOLRGAYGTVIMDSRHPDTLLAARSGLV 180
Db	121 SETDDEVIAHLVNWLKGCGTIREAVLAIPOLRGAYGTVIMDSRHPDTLLAARSGLV 180	Db	121 SETDDEVIAHLVNWLKGCGTIREAVLAIPOLRGAYGTVIMDSRHPDTLLAARSGLV 180
Qy	181 1IGLGNGENFIASDQLLIPVTRRFLEGGDIAETTRVNNIFDKTGAVSKRDIENLQ 240	Qy	181 1IGLGNGENFIASDQLLIPVTRRFLEGGDIAETTRVNNIFDKTGAVSKRDIENLQ 240
Db	181 1IGLGNGENFIASDQLLIPVTRRFLEGGDIAETTRVNNIFDKTGAVSKRDIENLQ 240	Db	181 1IGLGNGENFIASDQLLIPVTRRFLEGGDIAETTRVNNIFDKTGAVSKRDIENLQ 240
Qy	241 YDAGDKGIGIYRHYMKEIYEQPNAIKNTLGRISHQVDLSELGPNADELLSKVHEHQIILA 300	Qy	241 YDAGDKGIGIYRHYMKEIYEQPNAIKNTLGRISHQVDLSELGPNADELLSKVHEHQIILA 300
Db	241 YDAGDKGIGIYRHYMKEIYEQPNAIKNTLGRISHQVDLSELGPNADELLSKVHEHQIILA 300	Db	241 YDAGDKGIGIYRHYMKEIYEQPNAIKNTLGRISHQVDLSELGPNADELLSKVHEHQIILA 300
Qy	301 CGTSYNSGMVSYRNFYFESLAGIPCDVRIASEEPYRKSAYVRNSLMTLSQSETADLAGL 360	Qy	301 CGTSYNSGMVSYRNFYFESLAGIPCDVRIASEEPYRKSAYVRNSLMTLSQSETADLAGL 360
Db	301 CGTSYNSGMVSYRNFYFESLAGIPCDVRIASEEPYRKSAYVRNSLMTLSQSETADLAGL 360	Db	301 CGTSYNSGMVSYRNFYFESLAGIPCDVRIASEEPYRKSAYVRNSLMTLSQSETADLAGL 360
Qy	361 RLSKELGYLGSLSLACNVPSVLLRQESDLALMTNAGTEGVASVKAFTTQLTVLMLVAKL 420	Qy	361 RLSKELGYLGSLSLACNVPSVLLRQESDLALMTNAGTEGVASVKAFTTQLTVLMLVAKL 420
Db	361 RLSKELGYLGSLSLACNVPSVLLRQESDLALMTNAGTEGVASVKAFTTQLTVLMLVAKL 420	Db	361 RLSKELGYLGSLSLACNVPSVLLRQESDLALMTNAGTEGVASVKAFTTQLTVLMLVAKL 420
Qy	422 1SRLKGLDAS1EHDIVHGLALPSRTEQMSQDRIEALADFSDKHHAFLGRGDOYPIA 480	Qy	422 1SRLKGLDAS1EHDIVHGLALPSRTEQMSQDRIEALADFSDKHHAFLGRGDOYPIA 480
Db	422 1SRLKGLDAS1EHDIVHGLALPSRTEQMSQDRIEALADFSDKHHAFLGRGDOYPIA 480	Db	422 1SRLKGLDAS1EHDIVHGLALPSRTEQMSQDRIEALADFSDKHHAFLGRGDOYPIA 480
Qy	481 LEGALKLKELTSYIHAAYAAGEIKGHLPLALADMPVIVAPNNELEKLKSNIEEVBAR 540	Qy	481 LEGALKLKELTSYIHAAYAAGEIKGHLPLALADMPVIVAPNNELEKLKSNIEEVBAR 540
Db	481 LEGALKLKELTSYIHAAYAAGEIKGHLPLALADMPVIVAPNNELEKLKSNIEEVBAR 540	Db	481 LEGALKLKELTSYIHAAYAAGEIKGHLPLALADMPVIVAPNNELEKLKSNIEEVBAR 540
Qy	541 GGQLYVPAQDAGTVSSDMH1IEMPHEVEVIAPIFYTVPLQLLAYHVALKGTDVDQPR 600	Qy	541 GGQLYVPAQDAGTVSSDMH1IEMPHEVEVIAPIFYTVPLQLLAYHVALKGTDVDQPR 600
Db	541 GGQLYVPAQDAGTVSSDMH1IEMPHEVEVIAPIFYTVPLQLLAYHVALKGTDVDQPR 600	Db	541 GGQLYVPAQDAGTVSSDMH1IEMPHEVEVIAPIFYTVPLQLLAYHVALKGTDVDQPR 600
Qy	601 NLAKSVTVE 609	Qy	601 NLAKSVTVE 609
Db	601 NLAKSVTVE 609	Db	601 NLAKSVTVE 609
RESULT 2			
US-10-024-460-16			
; Sequence 16, Application US/10024460			
; Publication No US20030044939A1			
; GENERAL INFORMATION:			
; APPLICANT: Berry, Alan			
; APPLICANT: Burlingame, Richard P.			
; APPLICANT: Willis, James R.			
; TITLE OF INVENTION: PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE			
; FILE REFERENCE: 3161-18-CL			
; CURRENT FILING DATE: 2001-12-17			
; PRIORITY APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/115, 475			
; PRIORITY FILING DATE: 1998-07-15			
; PRIORITY APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035, 494			
; PRIORITY FILING DATE: EARLIER FILING DATE: 1997-01-14			
; NUMBER OF SEQ ID NOS: 31			
; SOFTWARE: Patentin Ver. 2.0			
; SEQ ID NO 16			
; LENGTH: 609			
; TYPE: PRT			
; ORGANISM: Escherichia coli			
US-10-024-460-16			
Query Match 100.0%; Score 3086; DB 4; Length 609;			
Best Local Similarity 100.0%; Pred. No. 4.7e-29; Mismatches 0; Indels 0; Gaps 0;			
Matches 609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1 MCGIVGATAQDVAEILLEGLRLEYGDSAGLAVDAEGHMTLRLRGKVMQLAQAAE 60	Qy	1 MCGIVGATAQDVAEILLEGLRLEYGDSAGLAVDAEGHMTLRLRGKVMQLAQAAE 60
Db	1 MCGIVGATAQDVAEILLEGLRLEYGDSAGLAVDAEGHMTLRLRGKVMQLAQAAE 60	Db	1 MCGIVGATAQDVAEILLEGLRLEYGDSAGLAVDAEGHMTLRLRGKVMQLAQAAE 60
Qy	61 EPLHGGTGIATRWAHGEPESEVNAHPVSEHIVVHNGIENHEPLREELKARGYTFV 120	Qy	61 EPLHGGTGIATRWAHGEPESEVNAHPVSEHIVVHNGIENHEPLREELKARGYTFV 120
RESULT 3			
US-10-369-493-23611			
; Sequence 23611, Application US/10369493			
; Publication No. US20033675A1			
; GENERAL INFORMATION:			
; APPLICANT: Cao, Yongwei			
; APPLICANT: Hinkle, Gregory J.			
; APPLICANT: Slater, Steven C.			
; APPLICANT: Goldman, Barry S.			
; APPLICANT: Chen, Xianfeng			
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES			
; FILE REFERENCE: 38-10 (52052) B			
; CURRENT APPLICATION NUMBER: US/10/369, 493			
; CURRENT FILING DATE: 2003-02-28			
; PRIOR APPLICATION NUMBER: US 60/360, 039			
; PRIOR FILING DATE: 2002-02-21			
; NUMBER OF SEQ ID NOS: 4774			
; SEQ ID NO 23611			
; LENGTH: 609			
; TYPE: PRT			
; ORGANISM: Escherichia coli			
US-10-369-493-23611			
Query Match 100.0%; Score 3086; DB 4; Length 609;			
Best Local Similarity 100.0%; Pred. No. 4.7e-29; Mismatches 0; Indels 0; Gaps 0;			
Matches 609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1 MCGIVGATAQDVAEILLEGLRLEYGDSAGLAVDAEGHMTLRLRGKVMQLAQAAE 60	Qy	1 MCGIVGATAQDVAEILLEGLRLEYGDSAGLAVDAEGHMTLRLRGKVMQLAQAAE 60
Db	1 MCGIVGATAQDVAEILLEGLRLEYGDSAGLAVDAEGHMTLRLRGKVMQLAQAAE 60	Db	1 MCGIVGATAQDVAEILLEGLRLEYGDSAGLAVDAEGHMTLRLRGKVMQLAQAAE 60
Qy	61 EPLHGGTGIATRWAHGEPESEVNAHPVSEHIVVHNGIENHEPLREELKARGYTFV 120	Qy	61 EPLHGGTGIATRWAHGEPESEVNAHPVSEHIVVHNGIENHEPLREELKARGYTFV 120

61 EPLHGGTGLAHTRWATHEPSEVNAHPVSEHIVVHNGIENHEPLREELKARGYTFV 120
 Db ; PRIOR FILING DATE: 2000-11-27
 Qy ; PRIOR APPLICATION NUMBER: 60/257,931
 121 SETDTEVIAHLVWELKQCGTLRPAVLRAIPOLRGAYGTIVMDSRHPDTLLAARSGSPLV 180
 Db ; PRIOR FILING DATE: 2000-12-22
 121 SETDTEVIAHLVWELKQCGTLRPAVLRAIPOLRGAYGTIVMDSRHPDTLLAARSGSPLV 180
 Db ; PRIOR APPLICATION NUMBER: 60/267,636
 181 IGLGMGENFTASDOLALLPTVTRRFLEGGDIAETTRSSVNIPDKTGAEVKRDIESNLQ 240
 Qy ; PRIOR FILING DATE: 2001-02-09
 181 IGLGMGENFTASDOLALLPTVTRRFLEGGDIAETTRSSVNIPDKTGAEVKRDIESNLQ 240
 Db ; Remaining Prior Application data removed - See File Wrapper or PALM.
 181 IGLGMGENFTASDOLALLPTVTRRFLEGGDIAETTRSSVNIPDKTGAEVKRDIESNLQ 240
 Qy ; NUMBER OF SEQ ID NOS: 78614
 241 YDAGDKGIVRHYMOKEIYQPNALKNTLGRISHQVDISLGPNADELLSKVHQLA 300
 Db ; SOFTWARE: PatentIn version 3.1
 241 YDAGDKGIVRHYMOKEIYQPNALKNTLGRISHQVDISLGPNADELLSKVHQLA 300
 Qy ; SEQ ID NO: 56753
 Db ; SBO ID: NO 56753
 241 LENGTH: 609
 Db ; TYPE: PRT
 Qy ; ORGANISM: Escherichia coli
 Us-10-282-12A-56753
 Qy ; Query Match 100.0%; Score 3086; DB 4; Length 609;
 Db Best Local Similarity 100.0%; Pred. No. 4.7e-249;
 Qy Matches 609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db Qy 1 MCGIVGAIAQRDVAEILLEGRRLRLEYRGSYDASGLAVVDAEGHNTRLRLGKVONLAQAAE 60
 Db 1 MCGIVGAIAQRDVAEILLEGRRLRLEYRGSYDASGLAVVDAEGHNTRLRLGKVONLAQAAE 60
 Qy 61 EPLHGGTGLIAHTRWATGEPSVNAHPVSEHIVVHNGIENHEPLREELKARGYTFV 120
 Db 61 EPLHGGTGLIAHTRWATGEPSVNAHPVSEHIVVHNGIENHEPLREELKARGYTFV 120
 Qy 61 EPLHGGTGLIAHTRWATGEPSVNAHPVSEHIVVHNGIENHEPLREELKARGYTFV 120
 Db 121 SETDTEVIAHLVWELKQCGTLRPAVLRAIPOLRGAYGTIVMDSRHPDTLLAARSGSPLV 180
 Qy 121 SETDTEVIAHLVWELKQCGTLRPAVLRAIPOLRGAYGTIVMDSRHPDTLLAARSGSPLV 180
 Db 121 SETDTEVIAHLVWELKQCGTLRPAVLRAIPOLRGAYGTIVMDSRHPDTLLAARSGSPLV 180
 Qy 181 IGLGMGENFTASDOLALLPTVTRRFIPLLEGDDIAETTRSSVNIPDKTGAEVKRDIESNLQ 240
 Db 181 IGLGMGENFTASDOLALLPTVTRRFIPLLEGDDIAETTRSSVNIPDKTGAEVKRDIESNLQ 240
 Qy 241 YDAGDKGIVRHYMOKEIYQPNALKNTLGRISHQVDISLGPNADELLSKVHQLA 300
 Db 241 YDAGDKGIVRHYMOKEIYQPNALKNTLGRISHQVDISLGPNADELLSKVHQLA 300
 Qy 301 CGTSGNSGMVSRWFESELAGIPCDVETIASEFRYRKSAYVRNSLMTLSQSGETADTLGL 360
 Db 301 CGTSGNSGMVSRWFESELAGIPCDVETIASEFRYRKSAYVRNSLMTLSQSGETADTLGL 360
 Qy 361 RLSKELGTYGSLAICNPGSSLVRESDLALMTNAGTEGVASTKAFTIQLTVMLVAKL 420
 Db 361 RLSKELGTYGSLAICNPGSSLVRESDLALMTNAGTEGVASTKAFTIQLTVMLVAKL 420
 Qy 421 SRLKGQDASIEHDIVHGLQALPSRIEQMLSQDRKIREALAEQDFSDKHHALFLGRGDQYTA 480
 Db 421 SRLKGQDASIEHDIVHGLQALPSRIEQMLSQDRKIREALAEQDFSDKHHALFLGRGDQYTA 480
 Qy 481 LEGALKLKKEISYTHAEAYAAGELKQPLALIDAMPVIVAPNNELELKLKSNEEYRAR 540
 Db 481 LEGALKLKKEISYTHAEAYAAGELKQPLALIDAMPVIVAPNNELELKLKSNEEYRAR 540
 Qy 541 GGQLYVFAQDAGFVSSDNMH1IEMPHYEVIAPIFYVPLQLAYHVALIKGTDYDQPR 600
 Db 541 GGQLYVFAQDAGFVSSDNMH1IEMPHYEVIAPIFYVPLQLAYHVALIKGTDYDQPR 600
 Qy 601 NLAKSVTE 609
 Db 601 NLAKSVTE 609
 RESULT 4
 US-10-282-12A-56753
 ; Sequence 56753, Application US/10282122A
 ; Publication No. US20040029129A1.
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangbu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari
 ; APPLICANT: Zyskind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Forsyth, R.
 ; APPLICANT: Xu, H.
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; FILE REFERENCE: ELITRA.034A
 ; CURRENT FILING DATE: 2003-02-20
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/230,335
 ; PRIOR FILING DATE: 2000-09-06
 ; PRIOR APPLICATION NUMBER: 60/230,347
 ; PRIOR FILING DATE: 2000-09-09
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625

RESULT 5
 US-10-612-779-2
 ; Sequence 2, Application US/10612779
 ; Publication No. US20040031976A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Deng, Ming-De
 ; APPLICANT: Angerer, J. David
 ; APPLICANT: Cyron, Don

RESULT 6

US-10-612-779-2.rapbm

US-10-823-397-23

Sequence 23, Application US/10823397

Publication No. US/0050042735A1

GENERAL INFORMATION:

APPLICANT: McMillin, Thomas B

APPLICANT: Ding, Ming-De

APPLICANT: Grund, Alan

TITLE OF INVENTION: Metabolic Engineering for Enhanced Production of Chitin and Chitosan in Microorganisms

FILE REFERENCE: 3161-18-3

CURRENT APPLICATION NUMBER: US/10/823,397

CURRENT FILING DATE: 2004-04-12

PRIOR APPLICATION NUMBER: 60/462,087

PRIOR FILING DATE: 2003-04-11

NUMBER OF SEQ ID NOS: 59

SOFTWARE: Patentin version 3.2

SEQ ID NO: 23

LENGTH: 609

TYPE: PRT

ORGANISM: Escherichia coli

US-10-823-397-23

Query Match 100.0%; Score 3086; DB 4; Length 609;

Best Local Similarity 100.0%; Pred. No. 4.7e-249;

Matches 609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCGIVGAIQRDVAELLLGLRRLERYGDSAGLAVDAEGMTLRLGKQMLQAAE 60

Db 1 MCGIVGAIQRDVAELLLGLRRLERYGDSAGLAVDAEGMTLRLGKQMLQAAE 60

Qy 61 EPLHGGTGAHTRWATGEPESEVNAHPHSEHIVVHNGIENHEPRLKARGYTFV 120

Db 61 EPLHGGTGAHTRWATGEPESEVNAHPHSEHIVVHNGIENHEPRLKARGYTFV 120

Qy 121 SETDPEVIAHLVNLKQGCTLREAVLAIPOLRGAYTIVMDSRHDPTLAAARGSSPLV 180

Db 121 SETDPEVIAHLVNLKQGCTLREAVLAIPOLRGAYTIVMDSRHDPTLAAARGSSPLV 180

Qy 121 SETDPEVIAHLVNLKQGCTLREAVLAIPOLRGAYTIVMDSRHDPTLAAARGSSPLV 180

Db 121 SETDPEVIAHLVNLKQGCTLREAVLAIPOLRGAYTIVMDSRHDPTLAAARGSSPLV 180

Qy 181 IGLGMGENFTASDQLALLPVTRRFIFLEGDDIAETTRSVNIFDKTGAEVKRDIESNLQ 240

Db 181 IGLGMGENFTASDQLALLPVTRRFIFLEGDDIAETTRSVNIFDKTGAEVKRDIESNLQ 240

Qy 241 YDAGDKGIVRHYMKETIYOPNAIKNTLGRISHQVDLSEGPNADELLSKVHIIQILA 300

Db 241 YDAGDKGIVRHYMKETIYOPNAIKNTLGRISHQVDLSEGPNADELLSKVHIIQILA 300

Qy 301 CGTTSYNSGMVSRWFEPLAGIPCDVETAEFRYRSKAVRNSLMTLSOSGETADTLAGL 360

Db 301 CGTTSYNSGMVSRWFEPLAGIPCDVETAEFRYRSKAVRNSLMTLSOSGETADTLAGL 360

Qy 361 RLSKELGYLGSLATCNYPGSSLYRESDLALMTNAGTIGVASTKAKFTTOLVLMVAKL 420

Db 361 RLSKELGYLGSLATCNYPGSSLYRESDLALMTNAGTIGVASTKAKFTTOLVLMVAKL 420

Qy 421 SRLKGLDASIEHDIVHGLQALPSRIEQMSQDKRIEALADEFSDKHHALFLGRDQYPTA 480

Db 421 SRLKGLDASIEHDIVHGLQALPSRIEQMSQDKRIEALADEFSDKHHALFLGRDQYPTA 480

Qy 481 LEGALKLKKEISYIHAAYAAGELKHPGLALIDAMPTIVVAPNNELEKKSNIEEVRAR 540

Db 481 LEGALKLKKEISYIHAAYAAGELKHPGLALIDAMPTIVVAPNNELEKKSNIEEVRAR 540

Qy 541 GGOLYVFAODQAGFVSSDNMHIEMPHVEVIAPIFYTVPLQLLAYHVALIKGTDVDQPR 600

Db 541 GGOLYVFAODQAGFVSSDNMHIEMPHVEVIAPIFYTVPLQLLAYHVALIKGTDVDQPR 600

Qy 601 NLAKSVTVE 609

Db 601 NLAKSVTVE 609

RESULT 7

US-10-024-460-28
 ; Sequence 28, Application US/10024460
 ; Publication No. US20030044939A1.

GENERAL INFORMATION:
 ; APPLICANT: Berry, Alan
 ; APPLICANT: Burlingame, Richard P.
 ; APPLICANT: Millis, James R.
 ; TITLE OF INVENTION: PROCES AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE
 ; FILE REFERENCE: 3161-18-CL
 ; CURRENT APPLICATION NUMBER: US/10/024, 460
 ; CURRENT FILING DATE: 2001-12-17
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/115, 475
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-15
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035, 494
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-14
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 28
 ; LENGTH: 609
 ; TYPE: PRT
 ; ORGANISM: Escherichia coli
 ; US-10-024-460-28

Query Match 99.8%; Score 3080; DB 4; Length 609;
 Best Local Similarity 99.8%; Pred. No. 1.5e-248; Indels 0; Gaps 0;
 Matches 608; Conservative 0; Mismatches 1; Gaps 0;

Qy 1 MCGIVGAIQRDVAEILLEGLRRLREYRGDSAGLAIVDDEAEGMTRRLRGKVQMLAQAE 60
 Db 1 MCGIVGAIQRDVAEILLEGLRRLREYRGDSAGLAIVDDEAEGMTRRLRGKVQMLAQAE 60
 Qy 61 EPHLGGTGIATHTWATHGPSEVNAHPVSEHIVVWNGIIEHNPREEELKARGYTFV 120
 Db 61 EPHLGGTGIATHTWATHGPSEVNAHPVSEHIVVWNGIIEHNPREEELKARGYTFV 120
 Qy 121 SETDTEVIAHLVNLKQCGTTLREAVRLAIPOLRGAYGTIVMDSRHPDTLLAARSGPV 180
 Db 121 SETDTEVIAHLVNLKQCGTTLREAVRLAIPOLRGAYGTIVMDSRHPDTLLAARSGPV 180
 Qy 181 IGLGMGENFTASDOLALIPVTRFIFLREGDIAETTRSVNIFDPTGAEVKRDIESNQ 240
 Db 181 IGLGMGENFTASDOLALIPVTRFIFLREGDIAETTRSVNIFDPTGAEVKRDIESNQ 240
 Qy 241 YDAGDKGIVRHMOKEIYEPNAIKNTLGRISHQVDSLSEGPNADELLSKYHIIQIA 300
 Db 241 YDAGDKGIVRHMOKEIYEPNAIKNTLGRISHQVDSLSEGPNADELLSKYHIIQIA 300
 Qy 301 CGTNSNMGVSRVTFESLAGIPCDVETASEFRYRSKAVRNLSMITSOSGETADTLAGL 360
 Db 301 CGTNSNMGVSRVTFESLAGIPCDVETASEFRYRSKAVRNLSMITSOSGETADTLAGL 360
 Qy 361 RLSKELGYLGLSLACNVPSLIVRESIDLALMTNGTEIGVASTKAFITQTLVMLVAKL 420
 Db 361 RLSKELGYLGLSLACNVPSLIVRESIDLALMTNGTEIGVASTKAFITQTLVMLVAKL 420
 Qy 422 SRLKGLDASLEHDIVHGLQALPSRLQOMISQDRIEALAEFSDKHHALFLGRGDQYPA 480
 Db 422 SRLKGLDASLEHDIVHGLQALPSRLQOMISQDRIEALAEFSDKHHALFLSRCDQYPA 480
 Qy 481 LEGALKLKKEISYIHAAYAAGELKGPLALIDADMPVIVAPNELLKLKSNTIEVRAR 540
 Db 481 LEGALKLKKEISYIHAAYAAGELKGPLALIDADMPVIVAPNELLKLKSNTIEVRAR 540
 Qy 541 GGOLYVFAODAGTVSSDNMHIITEMPHYEVIAPIFYTVPLQIAYHVLIKGTDVDQPR 600
 Db 541 GGOLYVFAODAGTVSSDNMHIITEMPHYEVIAPIFYTVPLQIAYHVLIKGTDVDQPR 600
 Qy 601 NLAKSVTVE 609
 Db 601 NLAKSVTVE 609

US-10-024-460-31
 ; Sequence 31, Application US/10024460
 ; Publication No. US20030044939A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Berry, Alan
 ; APPLICANT: Burlingame, Richard P.
 ; APPLICANT: Millis, James R.
 ; TITLE OF INVENTION: PROCES AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE
 ; FILE REFERENCE: 3161-18-CL
 ; CURRENT APPLICATION NUMBER: US/10/024, 460
 ; CURRENT FILING DATE: 2001-12-17
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/115, 475
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-15
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035, 494
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-14
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 31
 ; LENGTH: 609
 ; TYPE: PRT
 ; ORGANISM: Escherichia coli
 ; US-10-024-460-31

Query Match 99.8%; Score 3080; DB 4; Length 609;
 Best Local Similarity 99.8%; Pred. No. 1.5e-248; Indels 1; Gaps 0;
 Matches 608; Conservative 0; Mismatches 1; Gaps 0;

Qy 1 MCGIVGAIQRDVAEILLEGLRRLREYRGDSAGLAIVDDEAEGMTRRLRGKVQMLAQAE 60
 Db 1 MCGIVGAIQRDVAEILLEGLRRLREYRGDSAGLAIVDDEAEGMTRRLRGKVQMLAQAE 60
 Qy 61 EPHLGGTGIATHTWATHGPSEVNAHPVSEHIVVWNGIIEHNPREEELKARGYTFV 120
 Db 61 EPHLGGTGIATHTWATHGPSEVNAHPVSEHIVVWNGIIEHNPREEELKARGYTFV 120
 Qy 121 SETDTEVIAHLVNLKQCGTTLREAVRLAIPOLRGAYGTIVMDSRHPDTLLAARSGPV 180
 Db 121 SETDTEVIAHLVNLKQCGTTLREAVRLAIPOLRGAYGTIVMDSRHPDTLLAARSGPV 180
 Qy 181 IGLGMGENFTASDOLALIPVTRFIFLREGDIAETTRSVNIFDPTGAEVKRDIESNQ 240
 Db 181 IGLGMGENFTASDOLALIPVTRFIFLREGDIAETTRSVNIFDPTGAEVKRDIESNQ 240
 Qy 241 YDAGDKGIVRHMOKEIYEPNAIKNTLGRISHQVDSLSEGPNADELLSKYHIIQIA 300
 Db 241 YDAGDKGIVRHMOKEIYEPNAIKNTLGRISHQVDSLSEGPNADELLSKYHIIQIA 300
 Qy 301 CGTNSNMGVSRVTFESLAGIPCDVETASEFRYRSKAVRNLSMITSOSGETADTLAGL 360
 Db 301 CGTNSNMGVSRVTFESLAGIPCDVETASEFRYRSKAVRNLSMITSOSGETADTLAGL 360
 Qy 361 RLSKELGYLGLSLACNVPSLIVRESIDLALMTNGTEIGVASTKAFITQTLVMLVAKL 420
 Db 361 RLSKELGYLGLSLACNVPSLIVRESIDLALMTNGTEIGVASTKAFITQTLVMLVAKL 420
 Qy 421 SRLKGLDASLEHDIVHGLQALPSRLQOMISQDRIEALAEFSDKHHALFLGRGDQYPA 480
 Db 421 SRLKGLDASLEHDIVHGLQALPSRLQOMISQDRIEALAEFSDKHHALFLSRCDQYPA 480
 Qy 481 LEGALKLKKEISYIHAAYAAGELKGPLALIDADMPVIVAPNELLKLKSNTIEVRAR 540
 Db 481 LEGALKLKKEISYIHAAYAAGELKGPLALIDADMPVIVAPNELLKLKSNTIEVRAR 540
 Qy 541 GGOLYVFAODAGTVSSDNMHIITEMPHYEVIAPIFYTVPLQIAYHVLIKGTDVDQPR 600
 Db 541 GGOLYVFAODAGTVSSDNMHIITEMPHYEVIAPIFYTVPLQIAYHVLIKGTDVDQPR 600

4221	SRKGKDAS1EHDIYHGLQALPSREQMSQDKR1EALLDFSDKGHALFLS RDQYPA	480	Db	421	SRKGKDAS1EHDIYHGLQALPSREQMSQDKR1EALLDFSDKGHALFLS RDQYPA	480	Db
4811	LEGALKLKEISYIHAAYAAAGELKGPLALIDADMIVVAPNNELLEKLKSNI BEVRAR	540	Qy	481	LEGALKLKEISYIHAAYAAAGELKGPLALIDADMIVVAPNNELLEKLKSNI BEVRAR	540	Qy
4811	LEGALKLKEISYIHAAYAAAGELKGPLALIDADMIVVAPNNELLEKLKSNI BEVRAR	540	Db	481	LEGALKLKEISYIHAAYAAAGELKGPLALIDADMIVVAPNNELLEKLKSNI BEVRAR	540	Db
5411	GGOLYVFAODAGFVSSDNHHIEMPHVEVIAPIFYTPLQLLAYHVALIKGTPVDQPR	600	Qy	541	GGOLYVFAODAGFVSSDNHHIEMPHVEVIAPIFYTPLQLLAYHVALIKGTPVDQPR	600	Qy
5411	GGOLYVFAODAGFVSSDNHHIEMPHVEVIAPIFYTPLQLLAYHVALIKGTPVDQPR	600	Db	541	GGOLYVFAODAGFVSSDNHHIEMPHVEVIAPIFYTPLQLLAYHVALIKGTPVDQPR	600	Db
6011	NLAKSVTVE 609	609	Qy	601	NLAKSVTVE 609	609	Qy
6011	NLAKSVTVE 609	609	Db	601	NLAKSVTVE 609	609	Db
RESULT 11							
	US-10-024-460-25						
	Sequence 25 Application US/10024460						
	Publication No. US20040044939A1						
	GENERAL INFORMATION:						
	APPLICANT: Berry, Alan						
	APPLICANT: Burlingame, Richard P.						
	APPLICANT: Millis, James R.						
	FILE REFERENCE: 3161-18-CL						
	CURRENT APPLICATION NUMBER: US/10/024, 460						
	CURRENT FILING DATE: 2001-12-17						
	PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/115, 475						
	PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-15						
	PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035, 494						
	PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-14						
	NUMBER OF SEQ ID NOS: 31						
	SOFTWARE: PatentIn Ver. 2.0						
	SEQ ID NO: 25						
	LENGTH: 609						
	TYPE: PRT						
	ORGANISM: Escherichia coli						
	US-10-024-460-25						
Query Match							
Qy	Best Local Similarity 99.8%; Score 3079; DB 4; Length 609; Matches 608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;						
Qy	1 MCGIVGAI1QORDVAE1LLGCRRLREYRGYDSAGLAVIDAEGHMTRLRLKGVOMLAQAE 60						
Qy	1 MCGIVGAI1QORDVAE1LLGCRRLREYRGYDSAGLAVIDAEGHMTRLRLKGVOMLAQAE 60						
Qy	61 EHPHGGTGAHTWATGEPSVSEHVVNGI1ENHEPLBELKARGYTV 120						
Qy	61 EHPHGGTGAHTWATGEPSVSEHVVNGI1ENHEPLBELKARGYTV 120						
Qy	121 SETDTEVIAHLVNLKCGSTLREAVLRAIPOLRGAYGVIMDSRHPDTLAAARGSPLV 180						
Qy	121 SETDTEVIAHLVNLKCGSTLREAVLRAIPOLRGAYGVIMDSRHPDTLAAARGSPLV 180						
Qy	121.1 SETDTEVIAHLVNLKCGSTLREAVLRAIPOLRGAYGVIMDSRHPDTLAAARGSPLV 180						
Qy	121.1 SETDTEVIAHLVNLKCGSTLREAVLRAIPOLRGAYGVIMDSRHPDTLAAARGSPLV 180						
Qy	121.1.1 SETDTEVIAHLVNLKCGSTLREAVLRAIPOLRGAYGVIMDSRHPDTLAAARGSPLV 180						
Qy	181.1 IGLGMGENFTASDQLLIVTRRTRRFLEGDIABITRVSNI1F0KTGAEVKRDIESNLQ 240						
Qy	181.1 IGLGMGENFTASDQLLIVTRRTRRFLEGDIABITRVSNI1F0KTGAEVKRDIESNLQ 240						
Qy	181.1.1 IGLGMGENFTASDQLLIVTRRTRRFLEGDIABITRVSNI1F0KTGAEVKRDIESNLQ 240						
Qy	241.1 YDAGDKG1YRHMOKE1YOPNA1KNTLGR1S1QD1SELGNADELLSKVH1Q1LA 300						
Qy	241.1 YDAGDKG1YRHMOKE1YOPNA1KNTLGR1S1QD1SELGNADELLSKVH1Q1LA 300						
Qy	301.1 CGTTSYNSGMVSYRFNFESSLAGIPCDV1EASFRYRKSAYVNRSLIMITSOSGETADTLGL 360						
Qy	301.1 CGTTSYNSGMVSYRFNFESSLAGIPCDV1EASFRYRKSAYVNRSLIMITSOSGETADTLGL 360						
Qy	301.1.1 CGTTSYNSGMVSYRFNFESSLAGIPCDV1EASFRYRKSAYVNRSLIMITSOSGETADTLGL 360						
Qy	301.1.1.1 CGTTSYNSGMVSYRFNFESSLAGIPCDV1EASFRYRKSAYVNRSLIMITSOSGETADTLGL 360						
Qy	361.1 RLSKELGYGSLAI CNVPOSSLVRESDALMNTAGTEIGVASTKAFTTQLVLMVAKL 420						
Qy	361.1 RLSKELGYGSLAI CNVPOSSLVRESDALMNTAGTEIGVASTKAFTTQLVLMVAKL 420						
Qy	361.1.1 RLSKELGYGSLAI CNVPOSSLVRESDALMNTAGTEIGVASTKAFTTQLVLMVAKL 420						
Qy	361.1.1.1 RLSKELGYGSLAI CNVPOSSLVRESDALMNTAGTEIGVASTKAFTTQLVLMVAKL 420						
Qy	4221 SRKGKDAS1EHDIYHGLQALPSREQMSQDKR1EALLDFSDKGHALFLS RDQYPA						
Qy	4221 SRKGKDAS1EHDIYHGLQALPSREQMSQDKR1EALLDFSDKGHALFLS RDQYPA						

Db	181 IGLGMGENFIASDQLALLPVTRRFIFLEGGDIAETRRSVNIFDKTGAEVKRODIESNLQ 240	Db	181 IGLGMGENFIASDQLALLPVTRRFIFLEGGDIAETRRSVNIFDKTGAEVKRODIESNLQ 240
Qy	241 YDAGDKGIYRHYMOKEIVOPNAIKNTLIGRISHGQVDLSELGPNADELLSKYEHIQILA 300	Qy	241 YDAGDKGIYRHYMOKEIVOPNAIKNTLIGRISHGQVDLSELGPNADELLSKYEHIQILA 300
Db	241 YDAGDKGIYRHYMOKEIVOPNAIKNTLIGRISHGQVDLSELGPNADELLSKYEHIQILA 300	Db	241 YDAGDKGIYRHYMOKEIVOPNAIKNTLIGRISHGQVDLSELGPNADELLSKYEHIQILA 300
Qy	301 CGTSYNSGMVSRWFESELAGIPCDVEIAESFRYRKSAYVRNSLIMTUSQSGETADTLAGL 360	Qy	301 CGTSYNSGMVSRWFESELAGIPCDVEIAESFRYRKSAYVRNSLIMTUSQSGETADTLAGL 360
Db	301 CGTSYNSGMVSRWFESELAGIPCDVEIAESFRYRKSAYVRNSLIMTUSQSGETADTLAGL 360	Db	301 CGTSYNSGMVSRWFESELAGIPCDVEIAESFRYRKSAYVRNSLIMTUSQSGETADTLAGL 360
Qy	361 RLSKELGYLSLAICNVPOSSLVRESDLALMTNGTEGVASTKAFITQTLVLMVAKL 420	Qy	361 RLSKELGYLSLAICNVPOSSLVRESDLALMTNGTEGVASTKAFITQTLVLMVAKL 420
Db	361 RLSKELGYLSLAICNVPOSSLVRESDLALMTNGTEGVASTKAFITQTLVLMVAKL 420	Db	361 RLSKELGYLSLAICNVPOSSLVRESDLALMTNGTEGVASTKAFITQTLVLMVAKL 420
Qy	421 SRLKGLDASIEHDIVHGLQALPSRIEOMLSQDKRIEALAEFSDKHIALFLGRGDOYPIA 480	Qy	421 SRLKGLDASIEHDIVHGLQALPSRIEOMLSQDKRIEALAEFSDKHIALFLGRGDOYPIA 480
Db	421 SRLKGLDASIEHDIVHGLQALPSRIEOMLSQDKRIEALAEFSDKHIALFLGRGDOYPIA 480	Db	421 SRLKGLDASIEHDIVHGLQALPSRIEOMLSQDKRIEALAEFSDKHIALFLGRGDOYPIA 480
Qy	481 LEGALKLKEISYIHAEAAYAEGELKHGPLALIDADMPVIVAPNNEELKLSNIEYRAR 540	Qy	481 LEGALKLKEISYIHAEAAYAEGELKHGPLALIDADMPVIVAPNNEELKLSNIEYRAR 540
Db	481 LEGALKLKEISYIHAEAAYAEGELKHGPLALIDADMPVIVAPNNEELKLSNIEYRAR 540	Db	481 LEGALKLKEISYIHAEAAYAEGELKHGPLALIDADMPVIVAPNNEELKLSNIEYRAR 540
Qy	541 GGQLYVFAQQDAGFVSSDMHIIEMPHVEEVIAPIFYTVPLQLLAYHVALIKGTDVDQPR 600	Qy	541 GGQLYVFAQQDAGFVSSDMHIIEMPHVEEVIAPIFYTVPLQLLAYHVALIKGTDVDQPR 600
Db	541 GGQLYVFAQQDAGFVSSDMHIIEMPHVEEVIAPIFYTVPLQLLAYHVALIKGTDVDQPR 600	Db	541 GGQLYVFAQQDAGFVSSDMHIIEMPHVEEVIAPIFYTVPLQLLAYHVALIKGTDVDQPR 600
Qy	601 NLAKSVTVE 609	Qy	601 NLAKSVTVE 609
Db	601 NLAKSVTVE 609	Db	601 NLAKSVTVE 609
Search completed: August 7, 2006, 09:28:24			
Job time : 95 secs			
GENERAL INFORMATION:			
APPLICANT: Berry, Alan			
APPLICANT: Burlingame, Richard P.			
APPLICANT: Millis, James R.			
TITLE OF INVENTION: PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE			
FILE REFERENCE: 3161-18-CL			
CURRENT APPLICATION NUMBER: US10/024,460			
CURRENT FILING DATE: 2001-12-17			
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/115,475			
PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-15			
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035,494			
PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-14			
NUMBER OF SEQ ID NOS: 31			
SOFTWARE: PatentIn Ver. 2.0			
SEQ ID NO: 22			
LENGTH: 609			
TYPE: PCT			
ORGANISM: Escherichia coli			
US-10-024-460-22			
Query Match 99.4%; Score 3068; DB 4; Length 609;			
Best Local Similarity 99.5%; Prod. No. 1..5e-24; Mismatches 3; Indels 0; Gaps 0;			
Qy	1 MCGIVGAIJAQRDVAEILLEGRLRLEYRGDSAGLAVVDAEGHMTLRLRGKYMOLAQAE 60	Qy	1 MCGIVGAIJAQRDVAEILLEGRLRLEYRGDSAGLAVVDAEGHMTLRLRGKYMOLAQAE 60
Db	1 MCGIVGAIJAQRDVAEILLEGRLRLEYRGDSAGLAVVDAEGHMTLRLRGKYMOLAQAE 60	Db	1 MCGIVGAIJAQRDVAEILLEGRLRLEYRGDSAGLAVVDAEGHMTLRLRGKYMOLAQAE 60
Qy	61 EPHLHGCGTAIHRWATCPESEVNAHPVSEHIVVYNGIENHEPRLKARGTIV 120	Qy	61 EPHLHGCGTAIHRWATCPESEVNAHPVSEHIVVYNGIENHEPRLKARGTIV 120
Db	61 EPHLHGCGTAIHRWATCPESEVNAHPVSEHIVVYNGIENHEPRLKARGTIV 120	Db	61 EPHLHGCGTAIHRWATCPESEVNAHPVSEHIVVYNGIENHEPRLKARGTIV 120
Qy	121 SEDTDEVIAHLVWELKGQTLEAVRLAIPQRGAYTVIMSDRHPDILLARSGPLV 180	Qy	121 SEDTDEVIAHLVWELKGQTLEAVRLAIPQRGAYTVIMSDRHPDILLARSGPLV 180
Db	121 SEDTDEVIAHLVWELKGQTLEAVRLAIPQRGAYTVIMSDRHPDILLARSGPLV 180	Db	121 SEDTDEVIAHLVWELKGQTLEAVRLAIPQRGAYTVIMSDRHPDILLARSGPLV 180
Qy	181 IGLGMGENFIASDQLALLPVTRRFIFLEGGDIAETRRSVNIFDKTGAEVKRODIESNLQ 240	Qy	181 IGLGMGENFIASDQLALLPVTRRFIFLEGGDIAETRRSVNIFDKTGAEVKRODIESNLQ 240

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OM protein - protein search, using SW model

Run on: August 7, 2006, 09:27:53 ; Search time 156 Seconds
 (without alignments)

261.222 Million cell updates/sec

Title: US-10-612-779-2

Perfect score: 3086

Sequence: 1 MCGIVGAIAGORDVAILEG.....LIKGDVDQPRNLAKSVTVE 609

Scoring table: BL0SUM62

Gapext 0.5

Searched: 236815 seqs, 66914042 residues

Total number of hits satisfying chosen parameters: 236815

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications AA New:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/us09_new_pub.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/us06_new_pub.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/us07_new_pub.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/us08_new_pub.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/pc1_new_pub.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/us10_new_pub.pep:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/us11_new_pub.pep:*

8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/us60_new_pub.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARES

Result No.	Score	Query	Match length	DB	ID	Description
1	3086	100.0	609	7	US-11-245-473-16	Sequence 16, App1
2	3080	99.8	609	7	US-11-245-473-28	Sequence 28, App1
3	3080	99.8	609	7	US-11-245-473-31	Sequence 31, App1
4	3079	99.8	609	7	US-11-245-473-25	Sequence 25, App1
5	3071	99.5	609	7	US-11-245-473-19	Sequence 19, App1
6	3068	99.4	609	7	US-11-245-473-22	Sequence 22, App1
7	1150	37.3	601	6	US-10-471-571A-2268	Sequence 2268, App1
8	1109	35.9	681	6	US-10-480-021-6	Sequence 6, App1
9	1109	35.9	681	6	US-10-480-021-7	Sequence 7, App1
10	1103	5	35.8	682	6	US-10-480-021-8
11	1089	35.3	680	6	US-10-493-349-34174	
12	1078	34.9	697	6	US-10-449-902-38427	
13	808	26.2	491	6	US-10-953-349-34175	
14	807	26.2	488	6	US-10-953-349-34176	
15	589	5	19.1	464	6	US-10-488-015-17
16	557	5	18.1	286	6	US-10-449-902-36965
17	252	8.2	541	6	US-10-449-902-34059	
18	240	7.8	501	6	US-10-471-571A-5078	
19	222	5	7.2	563	7	US-11-330-403-6080
20	188	6.1	600	6	US-10-449-902-38704	
21	186	6.0	541	7	US-11-330-403-13759	
22	186	6.0	544	7	US-11-330-403-8689	
23	184	5.5	78	6	US-10-488-015-16	
24	183	5.9	610	7	US-11-330-403-1786	
25	183	5.9	525	7	US-11-330-403-17502	

ALIGNMENTS

RESULT 1
 US-11-245-473-16
 Sequence 16, Application US/11245473
 ; Publication No. US20060094085A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Berry, Alan
 ; INVENTOR: Burlingame, Richard P.
 ; APPLICANT: Millis, James R.
 ; TITLE OF INVENTION: PROCESSES AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE
 ; FILE REFERENCE: 3161-18-1
 ; CURRENT APPLICATION NUMBER: US/11/245,473
 ; CURRENT FILING DATE: 2005-10-05
 ; PRIORITY APPLICATION NUMBER: US/10/024,460
 ; PRIORITY FILING DATE: 2001-12-17
 ; PRIORITY APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/115,475
 ; PRIORITY FILING DATE: EARLIER FILING DATE: 1998-07-15
 ; PRIORITY APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035,494
 ; PRIORITY FILING DATE: EARLIER FILING DATE: 1997-01-14
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 16
 ; LENGTH: 609
 ; TYPE: PRT
 ; ORGANISM: Escherichia coli
 US-11-245-473-16

Query Match 100.0%; Score 3086; DB 7; Length 609;
 Best Local Similarity 100.0%; Pred. No. 9.8e-221;
 Matches 609; Conservative 0; Indels 0; Gaps 0;

QY 1 MCGIVGATAQDVAILEGLRLRLEYGVDAGEMTRRLRLGKVQMLAQAE 60
 DB 1 MCGIVGATAQDVAILEGLRLRLEYGVDAGEMTRRLRLGKVQMLAQAE 60

QY 61 EHPLGGTIAHTRWATHGEPESEVNAHPVSEHIVVHNGIENHEPRLKARYTV 120
 DB 61 EHPLGGTIAHTRWATHGEPESEVNAHPVSEHIVVHNGIENHEPRLKARYTV 120

QY 121 SETDEVIAHLYNWLKGOGTIREAVIPLPQURGAYGTIVMISRHPTDILAKRSGPLV 180
 DB 121 SETDEVIAHLYNWLKGOGTIREAVIPLPQURGAYGTIVMISRHPTDILAKRSGPLV 180

QY 181 IGLGMGENFIASDOLALLPVTRPFLLEGDIABITRASNIPDKTGAEVKRDIESNLQ 240
 DB 181 IGLGMGENFIASDOLALLPVTRPFLLEGDIABITRASNIPDKTGAEVKRDIESNLQ 240

QY 241 YDAGDKGTYRHYMOKETIEQPNIAKNTLGRISHQVDSLSEGPNADEBLSKYH1QIA 300

^RESULT 2
 US-11-245-473-28
 / Sequence 28, Application US/11245473
 / Publication No. US20060094085A1
 / GENERAL INFORMATION:
 / APPLICANT: Berry, Alan
 / APPLICANT: Burlingame, Richard P.
 / TITLE OF INVENTION: PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE
 / FILE REFERENCE: 3161-18-CL
 / CURRENT APPLICATION NUMBER: US/11/245,473
 / CURRENT FILING DATE: 2005-10-05
 / PRIORITY NUMBER: US/10/024,460
 / PRIORITY FILING DATE: 2001-12-17
 / PRIORITY NUMBER: EARLIER APPLICATION NUMBER: 09/115,475
 / PRIORITY FILING DATE: 1998-07-15
 / PRIORITY NUMBER: EARLIER APPLICATION NUMBER: 60/035,494
 / PRIORITY FILING DATE: 1997-01-14
 / NUMBER OF SEQ ID NOS: 31
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO: 28
 / LENGTH: 609
 / TYPE: PRT
 / ORGANISM: Escherichia coli
 / US-11-245-473-28

Query Match 99.8%; Score 3080; DB 7; Length 609;
 Best Local Similarity 99.8%; Pred. No. 2.7e-220;
 Matches 608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MCGIVGAIQRDVAELLEGRLREYGYDSAGLVDAEGIMTRRLGKVMLAQAAE 60
 Db 1 MCGIVGAIQRDVAELLEGRLREYGYDSAGLVDAEGIMTRRLGKVMLAQAAE 60
 Qy 61 EHPLHGGTCAIHTRWATGEPESEVNAHPHSEHIVVHNGTLEAHLVPLRELKARYTFV 120
 Db 61 EHPLHGGTCAIHTRWATGEPESEVNAHPHSEHIVVHNGTLEAHLVPLRELKARYTFV 120
 Qy 121 SETDTEVIAHLVNLWELKGQTLEAHLVPLRELKARYTFV 120
 Db 121 SETDTEVIAHLVNLWELKGQTLEAHLVPLRELKARYTFV 120
 Qy 181 IGLGMGENFIASDQLLPPVTRRFIFLEGDAEITRSVNTFDKTGAEVYRQDIESNLQ 240
 Db 181 IGLGMGENFIASDQLLPPVTRRFIFLEGDAEITRSVNTFDKTGAEVYRQDIESNLQ 240

Qy 241 YDAGDKGTYRHMQKEIYEOPNAIKNTLGRISHGQVDLSELGPNADELLSKVHEHQILA 300
 Db 241 YDAGDKGTYRHMQKEIYEOPNAIKNTLGRISHGQVDLSELGPNADELLSKVHEHQILA 300
 Qy 301 CGTSYNSGMSRYWFESSLAGIPCDVETASERYSRKAUTLTSQSSETADTLAGL 360
 Db 301 CGTSYNSGMSRYWFESSLAGIPCDVETASERYSRKAUTLTSQSSETADTLAGL 360
 Qy 361 RLSKELGYLGSLAICNVPGSSLVRBSDLALMNTAEGVASTRAFTTQLTVLMLVAKL 420
 Db 361 RLSKELGYLGSLAICNVPGSSLVRBSDLALMNTAEGVASTRAFTTQLTVLMLVAKL 420
 Qy 361 RLSKELGYLGSLAICNVPGSSLVRBSDLALMNTAEGVASTRAFTTQLTVLMLVAKL 420
 Db 361 RLSKELGYLGSLAICNVPGSSLVRBSDLALMNTAEGVASTRAFTTQLTVLMLVAKL 420
 Qy 421 SRLKGLDASIEHDIVHGLQALPSREQMLSQDKRTEALDFSDKHHALFLGRGDQYTA 480
 Db 421 SRLKGLDASIEHDIVHGLQALPSREQMLSQDKRTEALDFSDKHHALFLGRGDQYTA 480
 Qy 421 SRLKGLDASIEHDIVHGLQALPSREQMLSQDKRTEALDFSDKHHALFLGRGDQYTA 480
 Db 421 SRLKGLDASIEHDIVHGLQALPSREQMLSQDKRTEALDFSDKHHALFLGRGDQYTA 480
 Qy 481 LEGALKLKEIKEYSIHAAAYAAGELKGQPLALIDAMDEVVIVAPNNELEKLSNIEVRAR 540
 Db 481 LEGALKLKEIKEYSIHAAAYAAGELKGQPLALIDAMDEVVIVAPNNELEKLSNIEVRAR 540
 Qy 541 GGQLYVFAQDAGFVSSDNHIIEMPHVEETAPIFTYVPLQLLAYHVALKGTDVDQPR 600
 Db 541 GGQLYVFAQDAGFVSSDNHIIEMPHVEETAPIFTYVPLQLLAYHVALKGTDVDQPR 600
 Qy 541 GGQLYVFAQDAGFVSSDNHIIEMPHVEETAPIFTYVPLQLLAYHVALKGTDVDQPR 600
 Db 541 GGQLYVFAQDAGFVSSDNHIIEMPHVEETAPIFTYVPLQLLAYHVALKGTDVDQPR 600
 Qy 601 NLAKSVTVE 609
 Db 601 NLAKSVTVE 609
 Qy 601 NLAKSVTVE 609
 Db 601 NLAKSVTVE 609

RESULT 3
 US-11-245-473-31
 / Sequence 31, Application US/11245473
 / Publication No. US20060094085A1
 / GENERAL INFORMATION:
 / APPLICANT: Berry, Alan
 / APPLICANT: Burlingame, Richard P.
 / APPLICANT: Millis, James R.
 / TITLE OF INVENTION: PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE
 / FILE REFERENCE: 3161-18-CL
 / CURRENT APPLICATION NUMBER: US/11/245,473
 / CURRENT FILING DATE: 2005-10-05
 / PRIORITY NUMBER: US/10/024,460
 / PRIORITY FILING DATE: 2001-12-17
 / PRIORITY NUMBER: EARLIER APPLICATION NUMBER: 09/115,475
 / PRIORITY FILING DATE: 1998-07-15
 / PRIORITY NUMBER: EARLIER APPLICATION NUMBER: 60/035,494
 / PRIORITY FILING DATE: 1997-01-14
 / NUMBER OF SEQ ID NOS: 31
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO: 31
 / LENGTH: 609
 / TYPE: PRT
 / ORGANISM: Escherichia coli
 / US-11-245-473-31

Query Match 99.8%; Score 3080; DB 7; Length 609;
 Best Local Similarity 99.8%; Pred. No. 2.7e-220;
 Matches 608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MCGIVGAIQRDVAELLEGRLREYGYDSAGLVDAEGIMTRRLGKVMLAQAAE 60
 Db 1 MCGIVGAIQRDVAELLEGRLREYGYDSAGLVDAEGIMTRRLGKVMLAQAAE 60
 Qy 61 EHPLHGGTCAIHTRWATGEPESEVNAHPHSEHIVVHNGTLEAHLVPLRELKARYTFV 120
 Db 61 EHPLHGGTCAIHTRWATGEPESEVNAHPHSEHIVVHNGTLEAHLVPLRELKARYTFV 120
 Qy 121 SETDTEVIAHLVNLWELKGQTLEAHLVPLRELKARYTFV 120
 Db 121 SETDTEVIAHLVNLWELKGQTLEAHLVPLRELKARYTFV 120
 Qy 181 IGLGMGENFIASDQLLPPVTRRFIFLEGDAEITRSVNTFDKTGAEVYRQDIESNLQ 240
 Db 181 IGLGMGENFIASDQLLPPVTRRFIFLEGDAEITRSVNTFDKTGAEVYRQDIESNLQ 240

181 IGLGMGENFIASDQLALLPVTRRFIFLEGDIAETTRSYNIFDKTGAEVKRDIESNLQ 240
 Db Qy 181 IGLGMGENFIASDQLALLPVTRRFIFLEGDIAETTRSYNIFDKTGAEVKRDIESNLQ 240
 Qy 241 YDAGDKGIYRHMOKEIYEOPNAIKNTLGRISHGQVDLSELGPNADELLSKVHEIQLA 300
 Db 241 YDAGDKGIYRHMOKEIYEOPNAIKNTLGRISHGQVDLSELGPNADELLSKVHEIQLA 300
 Qy 301 CGTSYNSGMYSRYWPESSLAGIPCDVIAESEFRYKSAVRNSLMTLSOSGETADTLAGL 360
 Db 301 CGTSYNSGMYSRYWPESSLAGIPCDVIAESEFRYKSAVRNSLMTLSOSGETADTLAGL 360
 Qy 361 RLSKELGYLSSLAI CNVPESSLVRESDLALMTNAGTEIGVASTKAPTQTLVLMVAKL 420
 Db 361 RLSKELGYLSSLAI CNVPESSLVRESDLALMTNAGTEIGVASTKAPTQTLVLMVAKL 420
 Qy 421 SRLKGLDASIEHDIVHGLQALPSREQMLSDKREBALAEDFSDKHFAFLSRSQDQYPA 480
 Db 421 SRLKGLDASIEHDIVHGLQALPSREQMLSDKREBALAEDFSDKHFAFLSRSQDQYPA 480
 Qy 481 LEGALKLKEISYIHAAYAAGELKHGPLALIDAMPVIVAPNNELEKLSNTEEVRA 540
 Db 481 LEGALKLKEISYIHAAYAAGELKHGPLALIDAMPVIVAPNNELEKLSNTEEVRA 540
 Qy 541 GGOLYVFAODAGYFSSDNHIIEMPVTEEVIAPIFYTPLQLLAYHVALIKGTVDQPR 600
 Db 541 GGOLYVFAODAGYFSSDNHIIEMPVTEEVIAPIFYTPLQLLAYHVALIKGTVDQPR 600
 Qy 601 NLAKSVTVE 609
 Db 601 NLAKSVTVE 609
 Qy 601 NLAKSVTVE 609
 Db 601 NLAKSVTVE 609

RESULT 4
 US-11-245-473-25

Sequence 25, Application US/11245473
 Publication No. US20060094085A1
 GENERAL INFORMATION:
 APPLICANT: Berry, Alan
 APPLICANT: Burlingame, Richard P.
 APPLICANT: Millis, James R.
 TITLE OF INVENTION: PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE
 CURRENT APPLICATION NUMBER: US/11/245,473
 CURRENT FILING DATE: 2005-10-05
 PRIOR APPLICATION NUMBER: US/10/024,460
 PRIOR FILING DATE: 2001-12-17
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/115,475
 PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-15
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035,494
 PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-14
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 25
 LENGTH: 609
 TYPE: PRT
 ORGANISM: Escherichia coli

US-11-245-473-25

Query Match 99.8%; Score 3079; DB 7; Length 609;
 Best Local Similarity 99.8%; Pred. No. 3.2e-20;
 Matches 608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MCGIVGAIORDVAEILLEGURRLERYGDSAGLA VVDEAEGHMTLRLRGKVQMLAQAE 60
 Db 1 MCGIVGAIORDVAEILLEGURRLERYGDSAGLA VVDEAEGHMTLRLRGKVQMLAQAE 60
 Qy 61 EHPLHGGTGAHTRWATHGEPESEYNAHPHSEHTVVVNGI TIEHPEBELKARGYTFV 120
 Db 61 EHPLHGGTGAHTRWATHGEPESEYNAHPHSEHTVVVNGI TIEHPEBELKARGYTFV 120
 Qy 121 SETDTEVIAHLVNLKQGTLREAVLRAIPOLGAYGTIMOSRHPDTLAAARSGSPV 180
 Db 121 SETDTEVIAHLVNLKQGTLREAVLRAIPOLGAYGTIMOSRHPDTLAAARSGSPV 180

RESULT 5
 US-11-245-473-19

Sequence 19, Application US/11245473
 Publication No. US20060094085A1
 GENERAL INFORMATION:
 APPLICANT: Berry, Alan
 APPLICANT: Burlingame, Richard P.
 APPLICANT: Millis, James R.
 TITLE OF INVENTION: PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE
 CURRENT APPLICATION NUMBER: US/11/245,473
 CURRENT FILING DATE: 2005-10-05
 PRIOR APPLICATION NUMBER: US/10/024,460
 PRIOR FILING DATE: 2001-12-17
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/115,475
 PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-15
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035,494
 PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-14
 NUMBER OF SEQ ID NOS: 31
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 19
 LENGTH: 609
 TYPE: PRT
 ORGANISM: Escherichia coli

US-11-245-473-19

Query Match 99.5%; Score 3071; DB 7; Length 609;
 Best Local Similarity 99.5%; Pred. No. 1.3e-219;
 Matches 606; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MCGIVGAIQDVAEILLEGURRLERYGDSAGLA VVDEAEGHMTLRLRGKVQMLAQAE 60
 Db 1 MCGIVGAIQDVAEILLEGURRLERYGDSAGLA VVDEAEGHMTLRLRGKVQMLAQAE 60
 Qy 61 EHPLHGGTGAHTRWATHGEPESEYNAHPHSEHTVVVNGI TIEHPEBELKARGYTFV 120
 Db 61 EHPLHGGTGAHTRWATHGEPESEYNAHPHSEHTVVVNGI TIEHPEBELKARGYTFV 120
 Qy 121 SETDTEVIAHLVNLKQGTLREAVLRAIPOLGAYGTIMOSRHPDTLAAARSGSPV 180
 Db 121 SETDTEVIAHLVNLKQGTLREAVLRAIPOLGAYGTIMOSRHPDTLAAARSGSPV 180

Db 121 SETDTEVIAHLYNWEIKQGGTLREAVLRAIPQLRGAYGTVIMDSHPDDTLAARSGSPV 180
 Qy 181 IGLGMGENFIASDQLALLPVRREFLEEDIAETTRPSYNIEDTGAEKRODIESNQ 240
 Db 181 IGLGMGENFIASDQLALLPVRREFLEEDIAETTRPSYNIEDTGAEKRODIESNQ 240
 Qy 241 YDAGDKGIVRYHMQKETYEQPNIAKNTLTGRISHQVDSELGNADELLSKVEH1QIL 300
 Db 241 YDAGDKGIVRYHMQKETYEQPNIAKNTLTGRISHQVDSELGNADELLSKVEH1QIL 300
 Qy 301 CGTTSYNGMWSRYWFESLAGIPCDVEIASFRRYKSAVRNSLMTLSSQGETADTLGL 360
 Db 301 CGTTSYNGMWSRYWFESLAGIPCDVEIASFRRYKSAVRNSLMTLSSQGETADTLGL 360
 Qy 361 RLSKELGYLGSLAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFTTQLVILYAKL 420
 Db 361 RLSKELGYLGSLAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFTTQLVILYAKL 420
 Qy 421 SRLKGLDASIEHDIVGQALPSRFQMSQDKRTEALAEFSDKKHAKLFLGRGDQYPIA 480
 Db 421 SRLKGLDASIEHDIVGQALPSRFQMSQDKRTEALAEFSDKKHAKLFLGRGDQYPIA 480
 Db 421 SRLKGLDASIEHDIVGQALPSRFQMSQDKRTEALAEFSDKKHAKLFLGRGDQYPIA 480
 Qy 481 LEGALKLKEISYHAEAYAAGELRGPLALIDADMPVTVAPNELLKLSNIEETRAR 540
 Db 481 LEGALKLKEISYHAEAYAAGELRGPLALIDADMPVTVAPNELLKLSNIEETRAR 540
 Qy 541 GGQLTVFADODAGFVSSDNMHIITEMPHVEVIAPIFYTPLQLLAYVALIKSTDVQPR 600
 Db 541 GGQLTVFADODAGFVSSDNMHIITEMPHVEVIAPIFYTPLQLLAYVALIKSTDVQPR 600
 Qy 601 NLAKSVTVE 609
 Db 601 NLAKSVTVE 609
 Qy 601 NLAKSVTVE 609
 Db 601 NLAKSVTVE 609

RESULT 6
 US-11-245-473-22
 ; Sequence 22, Application US/11245473
 ; Publication No. US20060094085A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Berry, Alan
 ; APPLICANT: Burlingame, Richard P.
 ; APPLICANT: Millis, James R.
 ; TITLE OF INVENTION: PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE
 ; FILE REFERENCE: 3161-18-CL
 ; CURRENT APPLICATION NUMBER: US/11/245,473
 ; CURRENT FILING DATE: 2005-10-05
 ; PRIOR APPLICATION NUMBER: US/10/024,460
 ; PRIOR FILING DATE: 2001-12-17
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/115,475
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-15
 ; PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 60/035,494
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 22
 ; LENGTH: 609
 ; TYPE: PRT
 ; ORGANISM: Escherichia coli
 US-11-245-473-22

Query Match 99.4%; Score 3068; DB 7; Length 609;
 Best Local Similarity 99.5%; Pred. No. 2.1e-219; 0; Mismatches 3; Indels 0; Gaps 0;

Db 1 MCGIVGAIQRDVAEILLEGRLRLEYRGDSAGLAVDAEGHMTTRRLGKVQMLAQAAE 60
 Qy 1 MCGIVGAIQRDVAEILLEGRLRLEYRGDSAGLAVDAEGHMTTRRLGKVQMLAQAAE 60
 Db 1 MCGIVGAIQRDVAEILLEGRLRLEYRGDSAGLAVDAEGHMTTRRLGKVQMLAQAAE 60
 Qy 61 EPLHGGTGAIAHTRWATHGEPSVEVNAHPVSEH-IVVWNGLIEHENPRLREELKARGY 118
 Db 60 SSDFPDPVGIGHTWRATHGVPNHNHSFPHQSSNGRTFLVHNGVIENTEELKGEY-LQGYS 118
 Qy 119 FVSETDTEVIAHLYNWEIKQGGTLREAVLRAIPQLRGAYGTVIMDSHPDDTLAARSGSP 178
 Db 119 FVSETDTEVIVQLVEFSNQGLSTEAFKTVSLHGSYALGLDADKDVTIVAKNSP 178

QY 179 LVIGLGMGENFIASDOLALLPVTRRFIFIEEGDIAEITRRSYNIFDKTGAEVKRQDISSN 238
 Db 179 LLLGEGEFGVIVIASDALAMQVTSYKEHDHEVIVKDEVIKDDANVVERDSYAE 238

QY 239 LOYDGDKGKLYRHYNOKEIYQOPNAIKNTL----TGRISHGQVDSLGPNADELLSK 292
 Db 239 IDASDAEKGYAAYHMLKEHQEPAMRMRIQEYQDAEGLNKLKDQDINID----TKE 290

QY 293 VEHTOILACETSYNSGMVSYWFSRFLAGIPCDVEJASERPRYRSAVRNSLMTLSQSCB 352
 Db 291 ADRIYVIAACTSYAGLVGEFLEKWAQPTEVHASEFVNMPPLSERPLFVYISQSCB 350

QY 353 TADTLAIGRLSKELGYLSAICNVPGSVLRESDLMNTNAGTEIGVASTRAKFTTOLY 412
 Db 351 TADSAVVLVETNKUGH-KSITITAVGATSVREADHTLLHAGBIAVASTRAKTAQIAV 409

QY 413 LMLVAKLSRLKGDLASDIEHIVGLOQAPSRIQMLSDQKRIBALAEFSD-KHHALFL 471
 Db 410 LSLSLQIVAKXEHGREADI--DLRLRELAKVTTATEAVDADPIMQIATFLECTRNPPI 467

QY 472 GRGDQDPIALEGALKLKEYSYIHAAYAGELKHGPLAIIADADNPVIVAPNNELEKK 531
 Db 468 GRTIDYNSVLEGALKLKEYSYIQAEGFAGQELRGHTIAIEGTPVUGLATOKEVNLNSR 527

QY 532 SNTIEFVRARCGOLYVFAODDAGFVSSDNHHIEMPHVEVIAPIFTYVPLQYVHAI 591
 Db 528 GNVKEVVAHPCITSM--GLEKEGDTVI--PHVHBLTPVLSWVQLSYAAH 583

QY 592 KGTDVDQPRNLAKSIVTE 609
 Db 584 RDLDVDQPRNLAKSIVTE 601

RESULT 8
 ; Sequence 6, Application US/10480021
 ; Publication No. US20060121457A1
 ; GENERAL INFORMATION:
 ; APPLICANT: EXELIXIS, INC.
 ; TITLE OF INVENTION: GFATs AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
 ; CURRENT APPLICATION NUMBER: US/10/480,021
 ; CURRENT FILING DATE: 2003-12-04
 ; PRIOR APPLICATION NUMBER: US 60/295,076
 ; PRIOR FILING DATE: 2001-06-05
 ; PRIOR APPLICATION NUMBER: US 60/328,605
 ; PRIOR FILING DATE: 2001-10-10
 ; PRIOR APPLICATION NUMBER: US 60/357,253
 ; PRIOR FILING DATE: 2002-02-15
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 6
 ; LENGTH: 681
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-480-021-6

Query Match 35.9%; Score 1109; DB 6; Length 681;
 Best Local Similarity 38.0%; Pred. No. 4.2e-74; Indels 82; Gaps 14;
 Matches 261; Conservative 121; Mismatches 222; Score 1109; DB 6; Length 681;
 Query Match 35.9%; Score 1109; DB 6; Length 681;
 Best Local Similarity 38.0%; Pred. No. 4.2e-74; Indels 82; Gaps 14;

QY 1 MCGIVGAI----AQRDYBAILLEGLRLREYRGYDSAGLAV----VDAEGRMTR--L 46
 Db 1 MCGIVGAI----AQRDYBAILLEGLRLREYRGYDSAGLAV----VDAEGRMTR--L 46
 1 MCGIVGAI----AQRDYBAILLEGLRLREYRGYDSAGLAV----VDAEGRMTR--L 46
 1 MCGIVGAI----AQRDYBAILLEGLRLREYRGYDSAGLAV----VDAEGRMTR--L 46

QY 47 RRLGRVQMLQQAAS----EPLHAGGTGIAHTRWTHGEPESEVNPHVSE--HI 94
 Db 61 KKKGRVKAQDDEVHKQDMQDIEFDVH--LGIAHTRWATHGEPSVNSHPQRSDKNEF 118

QY 95 VVWINGIILTHEPPEELKARGTIVFVSESETDETEV AHLVNNW---ELKQGTLREAVLRAI 150
 Db 119 IVIHINGITRTNYKDLKFKLLESKYDQESEDTETIAKLVCKMYDNRRESQTSFTLVERV 178

QY 151 POLRGAYGTVIMDSRHPDTLLAARSGSPLVIGLGMG-----186
 Db 179 QQJEGAFALVFKSVHFFGQAVGTRGSPPLIGRSEHKLSTDHIPILYRTGDKGKSCNL 238

QY 187 -----ENFIASDQLALLPVTRRFIFLEGDIAEIT--RSVNFIDKNG 227
 Db 239 SRVDSITCLFPVKEAVYYFASDASAVIETHNTRVIFLEDDVVAVVDGRSLTHRKRTA 298

QY 228 AEYKRQDIESLNQVDAGD--KGLYRHYNOKEIYEQPNALKNTLGRISHQVDSLSELGPN 285
 Db 299 GDHPGRAVQT-LQMLEQQIMKGKGNFSMKEIIFOQEPESVNTNMRGRVNFDYTNN-LGSL 356

QY 286 ADEL--LSKVEHIOILACGTSYNSGKSYWFESLAGIPCDVEIASEFYRKSAVRNSL 433
 Db 357 KDHKEIQCRRLIACTSYHAGVATQVBLBEITLPVNEVLSDFLDRLNTPVRDDV 416

QY 344 MITLSQSGETADTLAIGRLSKELGYLSAICNVPGSVLRESDLMNTNAGTEGVAST 403
 Db 417 CFFLSQSGETADTLMLGRYCKERGAL-TVGITNTVGSISRETDGVHINAGPELGVAST 475

QY 404 KAFPTQLTVMLVAKLSPLKGLDASIEHDVHQLQALSRSRIBNQLSDQKRIBAEDPS 463
 Db 476 KATTSQFVSLVMFALLMMCDRISMQERKEIMLKJRKPLIKEVLSMDEIQKALATELY 535

QY 464 DKHHALFLGRGDOYPALEGALKLKEYSYIHAAYAGELKHGPLAIIADAMPVYVAPN 523
 Db 536 HQKSVLIMGRGYHTACLEGALKLKEYSYIHAAYAGELKHGPLAIIADAMPVYVAPN 595

QY 524 NELLEKLKSNTIEYARGQOLYYFADQDAGFVSSDNHHIEMPHVEEVAPIFYVPLQ 583
 Db 596 DHTYAKCQNALQQVVARQRPVYTCDEDTETIKNTKRTKIVPHSVDQCLQGILSVPLQ 655

QY 584 LATHVALIKGTDVDPQPRNLAKSIVTE 609
 Db 656 LAFHLAVLRLGYDVFDPRNLAKSIVTE 681

RESULT 9
 US-10-480-021-7
 Sequence 7, Application US/10480021
 ; Sequence 7, Application US/10480021
 ; Publication No. US20060121457A1
 ; GENERAL INFORMATION:
 ; APPLICANT: EXELIXIS, INC.
 ; TITLE OF INVENTION: GFATs AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
 ; FILE REFERENCE: EX02-068
 ; CURRENT APPLICATION NUMBER: US/10/480,021
 ; CURRENT FILING DATE: 2003-12-04
 ; PRIOR APPLICATION NUMBER: US 60/295,076
 ; PRIOR FILING DATE: 2001-06-05
 ; PRIOR APPLICATION NUMBER: US 60/328,605
 ; PRIOR FILING DATE: 2001-10-10
 ; PRIOR APPLICATION NUMBER: US 60/357,253
 ; PRIOR FILING DATE: 2002-02-15
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 7
 ; LENGTH: 681
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-480-021-7

Query Match 35.9%; Score 1109; DB 6; Length 681;
 Best Local Similarity 38.0%; Pred. No. 4.2e-74; Indels 222; Mismatches 261; Conservative 121; Mi smatches 222; Score 1109; DB 6; Length 681;

QY 1 MCGIVGAI----AQRDYBAILLEGLRLREYRGYDSAGLAV----VDAEGRMTR--L 46
 Db 1 MCGIVGAI----AQRDYBAILLEGLRLREYRGYDSAGLAV----VDAEGRMTR--L 46
 1 MCGIVGAI----AQRDYBAILLEGLRLREYRGYDSAGLAV----VDAEGRMTR--L 46

QY 47 RRLGRVQMLQQAAS----EPLHAGGTGIAHTRWTHGEPESEVNPHVSE--HI 94
 Db 61 KKKGRVKAQDDEVHKQDMQDIEFDVH--LGIAHTRWATHGEPSVNSHPQRSDKNEF 118

QY 47 RRUGKQMLQQAAS----EPLHAGGTGIAHTRWTHGEPESEVNPHVSE--HI 94
 Db 61 KKKGRVKAQDDEVHKQDMQDIEFDVH--LGIAHTRWATHGEPSVNSHPQRSDKNEF 118

95 VVWNGIENHEPRLRELLKARGYTFVSESTDTEVIAHLVNW---ELKQCGTLLREAVLRAI 150
 Qy 119 IVTHNGITTYKDKLKEFLKEFLKGFYDFESETTETAKLYCXMNDRESQTTFTLVERVI 178
 Db 151 PQLRGAYGTIVMDSSHPTDULLAARSGSPLVIGLNG--- 186
 Qy 179 QLEGAFAVLFVKSVHFPQAVGTRGSPLLIGVSEHKLSTDHPILYRTGDKKGSCNL 238
 Qy 187 -----ENFTASDOLALLPVTRREFLFEFGDIAETI--RSYNTNEDKIG 227
 Db 239 SRVDSTTCLPVEEKAVETYFASDASAVEHTNRTVFLFDDYVAWDGRSLTHRIKTA 298
 Qy 228 AEVRQDIESNLQYDAGD--KGIVRHYHMGKEIYQPNALKNTLTGRISHQGDLSGP 285
 Qy 299 GDHPERAVQYQ-LOMLOQIMKGNSNSFPMKEIFFQEPESVNTMGRYKNEFDDTYN-LGG 356
 Qy 286 ADEL--LSKVEHIIQTLACGTNSCMWSYXWFESLAGIFCDVETASFRYKSAVRENS 343
 Qy 357 KDHKEIQRCCRLLIIACGTSYHAGVATQVLELTLEVMEVLAISLDLDRNTPVFRDD 416
 Qy 344 MITLQSOSGETADTLAGLRLSKELKGYLSLAICHNYPGSILVRESDALMTNASTEIGVAST 403
 Db 417 CFFLQSOSGETADTLGLRCKERSAL-TGTTNTVGSSS-SRETDGVAHINAGPEIGVAST 475
 Qy 404 KAFTTQLTWILMLVAKLSRKLQGDLASIEHDIVHGLQALPSRQIMLSOKRKEALADES 463
 Db 476 KAYTSQFVSFVW 535
 Qy 466 DKHHALFLGRGDDQYPIALSGALKUKEISWTHAEAYAAGELKGKPLAIDADMVIVVAPN 523
 Db 536 HQKSVLIMGRGYHYATCLEGALKIKEITYMHSEGILAKGKPLAIDKLMPVIMIMR 595
 Qy 524 NELLEKLKSNTEYVRRGGOLYYFADODGFVSSDNMHJIEMPHVEEYIAPIFYTYPQL 583
 Db 596 DHTYAKCQNAQQLQVVARQRPVVICDKEPTETIKNTKRTKIVBHSVDCLQGILSVIPLQ 655
 Qy 584 LAYHALIKGTDYDQPRNLAKSFTVE 609
 Db 656 LAFHFLAVLRYGYDVFPRNLAKSFTVE 681
 Qy 647 GILSVTIPQQLSPHLAVLRYGYDVFPRNLAKSFTVE 682
 RESULT 10
 US-10-480-021-8
 ; Sequence 8, Application US/10480021
 ; Publication No. US20060121457A1
 ; GENERAL INFORMATION:
 ; APPLICANT: EXELIXIS, INC.
 ; TITLE OF INVENTION: GFATS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
 ; FILE REFERENCE: EX0-068
 ; CURRENT APPLICATION NUMBER: US/10/480, 021
 ; CURRENT FILING DATE: 2003-12-04
 ; PRIOR APPLICATION NUMBER: US 60/296, 076
 ; PRIOR FILING DATE: 2001-06-05
 ; PRIOR APPLICATION NUMBER: US 60/328, 605
 ; PRIOR FILING DATE: 2001-10-10
 ; PRIOR APPLICATION NUMBER: US 60/357, 253
 ; PRIOR FILING DATE: 2002-02-15
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 8
 ; LENGTH: 682
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-480-021-8
 Query Match 35.8%; Score 1103.5; DB 6; Length 682;
 Best Local Similarity 37.9%; Pred. No. 1..1e-73;
 Matches 264; Conservative 118; Mismatches 213; Indels 101; Gaps 14;
 Qy 1 MCGIVGAI-----AQDVAEIILLEGRLRUEYRGYDAGLAVD----AIGHMTRLRR 49
 Db 1 MCGIFPAYNNYRVRTRKEFETIQLGQRLTFRYDSAGAIDGNHHEVKERHIOQLVKKR 60
 Qy 50 GKVQMAQAA-----BEPDLHGGTGTIAHTRWATHGEPSVNAHPHVS---HI 94
 Db 61 GKVQMAQAA-----BEPDLHGGTGTIAHTRWATHGEPSVNAHPHVS---HI 115
 Qy 95 VVWNGIENHEPRLRELLKARGYTFVSESTDTEVIAHLVNW---KQGGLTREAVLRAI 150
 Db 116 VVWNGIENHEPRLRELLKARGYTFVSESTDTEVIAHLVNW---KQGGLTREAVLRAI 175
 Qy 151 PQLRGAYGTIVMDSSHPTDULLAARSGSPLVIGL 183
 Db 176 QOLEGAFALPVKSVHPEAVATRRSPLLIGVRSKYLSTEQIPLYRTCTLENVNIC 235
 Qy 184 -----GNG---ENFLASDQDALLPVTRRFIFLEGQIAETTRSVNIFDK 225
 Db 236 KTRMRKLDSSACLHAGDKAVERFPPSDASIIETMVRFLLEDIAAVADGKLSIH- 293
 Qy 226 TGAEVTR-----QDIESNLQYDAGDKGTYRHYMOKETIYEOPNAIKNTLTGRISHG 275
 Db 294 --RVRSASDPPSRAIQTLOMLOQIM--KGNFSFPMQEKEFQEVSVENTMGRVNF- 347
 Qy 276 QVDLSSIGPNADEL-LSKVHEHIIQIACCTSYNSGMSVSYWFEFLAGIIPCDVEIASFRY 333
 Db 348 RNTVILGGLKDHKEIRRCLLIVGCGTISYHAAVATRQVLEELTELPWVNEALASDFLD 407
 Qy 334 RKSAAVNRNSLMTLSOSGETADTLGLRSLKEGLGSLAICNVPGSSLYRESDALMTN 393
 Db 408 RNTPVERPDDYCEFFISGSGETADTLGLRSLKEGLGSLAICNVPGSSLYRESDALMTN 466
 Qy 394 AGTEIGVASTKAFTTOLVILMVALRSRGLDASIEHDIVHGLQALPSRTEQMSQDK 453
 Db 467 AGPEIGVASTKAFTTOLVILMVALRSRGLDASIEHDIVHGLQALPSRTEQMSQDK 526
 Qy 454 RIEALAEFDSKDHKHALFLGRGDDQYDIALEGALKLKEISYTHAEAYAAGELKGKPLAID 513
 Db 527 KIHDLALELTQRSLLVGMGYNATCLEGALKIKEITYMHSEGILAKGKPLAID 586
 Qy 514 DMPPVITVAPNNELELKSNEIEVBRGGQLYFADODGFVSSDNMHILEMPHVEVIA 573
 Db 587 QMPVNMVIMKMDOPCPFCARCONQLOQYARQGPILICSKDDOTESSKPKAYTIELPHTYDCLQ 646
 Qy 574 PIFYTVPOLLAYHVALLIKGTDYDOPRNLAKSFTVE 609
 Db 647 GILSVTIPQQLSPHLAVLRYGYDVFPRNLAKSFTVE 682
 RESULT 11
 US-10-953-349-34174
 ; Sequence 34174, Application US/10953349
 ; Publication No. US20060107345A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ALEXANDROV, NICKOLAI et al.
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 ; FILE REFERENCE: 2750-1579PUS2
 ; CURRENT APPLICATION NUMBER: US/10/953, 349
 ; CURRENT FILING DATE: 2004-09-30
 ; NUMBER OF SEQ ID NOS: 4025
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO: 4025
 ; SBQ ID NO: 34174
 ; TYPE: PRT
 ; ORGANISM: Zea mays subsp. mays
 ; US-10-953-349-34174
 Query Match 35.3%; Score 1089.5; DB 6; Length 680;
 Best Local Similarity 33.9%; Pred. No. 1..2e-72;
 Matches 253; Conservative 123; Mismatches 228; Indels 81; Gaps 15;
 Qy 1 MCGIVGAI-----AQDVAEIILLEGRLRUEYRGYDAGLAVD----AIGHMTR----- 45
 Db 1 MCGIFPAYNNYRVRTRKEFETIQLGQRLTFRYDSAGAIDGNHHEVKERHIOQLVKKR 59
 Qy 46 -----LRLGCKVQMLAQAAEHH-----PLHGGTGTIAHTRWATHGEPESS 83

1 MCGIVGAI---AQRD---VAEILLEGRLRERGRYDSAGLAV-VDAEGHMTRLRLRGKVQ 53
 1 MCGIFGYNLYVERKDFKILDTLVLGSRLETRGRYDSAGVADQDKNEVFAVEKGKV 60

1 MCGIAEEHPP---LHGGTGIAHTRWATHGRGPSEVNAHPhySE---HIVVYNGIEN 104
 1 KLIQOLIEEKPKDLTKFEDNHAGIAHTRWATHGPSPRNCHPHRSDPKWEFAVHNGLTN 120

54 MLIQAAEEHPP---LHGGTGIAHTRWATHGRGPSEVNAHPhySE---HIVVYNGIEN 104
 61 KLIQOLIEEKPKDLTKFEDNHAGIAHTRWATHGPSPRNCHPHRSDPKWEFAVHNGLTN 120

61 KLIQOLIEEKPKDLTKFEDNHAGIAHTRWATHGPSPRNCHPHRSDPKWEFAVHNGLTN 120

105 HEPREELKARGYFVSETDTEVIAHLYNWLKGQTLL--REAVYRALPQLRGAYGTIVM 162
 121 YKEVLVLESKGMRFETEDTEIAKLAKEVPLVAKVKELEGAGFLMLK 180

163 DSRHPDTLJAARSSESPVIGL-----183

181 SVRHPGEVVAARKSPLVGVAKMVKDVEYADGQALPAAASHNVALKGNDL 240

184 -----GM---GENPIASDOLALLPVTRRPFIFLEGDIARI 215

241 LSYVGLSADKSLLHRSQSRALSDDGMPQPTEPFLSSDPSAITEHTKCVLYEDDDIAHI 300

216 TRSVNIF----DTKGAEVKRDODIESNLQYDAGDKGTYRHYNQKEIVEQPNIAKNTLG 270

301 HEGOLNIHRLSLKTDDTSNVRAIQTEIEQLEQIM -KGKFDHNEQKEIPEQESIVNAARG 358

271 RISHQVDSLSEGPNADE-----LISKEVH7QIQLAGTSYNSGMSYRSGMVS 317

359 RL-----NAEKTVTUJLGRLQYISTIRRCRRLJIACTSYHSCMAVGAPE 406

318 LAGIPCDVIASEFRYRKSAVRNNSMLTQSGETADTLAQLRLSKELGYLGLSALCNV 377

407 LTEPIVSLASDPLDRQAPVFRDDTCVFSQSGETADSLMALRYCLERGAL-TVGVNV 465

378 PGSSLVRSSEDLALMNTAGTEIGVASTRAFTTQLTVLMLVAKUSRLKGLDASLTDHIVG 437

466 VGSSISLMLTHCGVHNAGPEIGVASTRAFTSQFVCMINFALTSDRASKTKQKLEMEG 525

438 LQALPSRTEQMLSDQDKRTEAFLDSFGKHALPFLGRGDOYPALEGALKLKEISYHAA 497

526 LSKISBQPRBLKUDQSIKEMCUKPDKOKSLLJGRGSOHATAGALKLKEISYHCEA 585

498 YANGELKHGPALIADMPVIVVAPPNELLEKLUKSNIBEVRAGQQLYFADQDAGFVSS 557

586 VMSGEELKHGPALVDENLPIVMLTRDTSIKA5LNAYQVIAKGRP1IVCNQDDEFFG 645

558 DNHHI1EMPHVEEVIAPIPYTVPLQLAYHVALIKGTQDQPNLAKSVTVE 609

646 EKTDKIEVPHTHELLQGLINVIPLQMLAYWLAVAEGLNVDPRNLAKSVTVE 697

Query Match 26.2%; Score 808; DB 6; Length 491;
 Best Local Similarity 36.7%; Pred. No. 5.2e-52;
 Matches 181; Conservative 98; Mismatches 182; Indels 32; Gaps 7;
 Type: PRT ; Organism: Zea mays subsp. may8

US-10-953-349-34175 Application US/10953349
 ; Publication No. US2006101745A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ALEXANDROV, Nickolai et al.
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 ; TITLE OF INVENTION: ENCODED THEREBY
 ; FILE REFERENCE: 2750-1579PUS2
 ; CURRENT APPLICATION NUMBER: US/10/953,349
 ; CURRENT FILING DATE: 2004-09-30
 ; NUMBER OF SEQ ID NOS: 40252
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 34175
 ; LENGTH: 491
 ; TYPE: PRT
 ; ORGANISM: Zea mays subsp. may8

RESULT 12
 US-10-449-902-38427
 Sequence 38427, Application US/10449902
 Publication No. US200612350A1

GENERAL INFORMATION:
 ; APPLICANT: National Institute of Agrobiological Sciences.
 ; APPLICANT: Bio-oriented Technology Research Advancement Institution.
 ; APPLICANT: The Institute of Physical and Chemical Research.
 ; APPLICANT: Foundation for Advancement of International Science.
 ; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
 ; FILE REFERENCE: MOA-A0205Y1-US
 ; CURRENT APPLICATION NUMBER: US/10/449,902
 ; CURRENT FILING DATE: 2003-05-29
 ; PRIORITY APPLICATION NUMBER: JP 2002-203269
 ; PRIORITY FILING DATE: 2002-05-30
 ; PRIORITY APPLICATION NUMBER: JP 2002-383870
 ; PRIORITY FILING DATE: 2002-12-11
 ; NUMBER OF SEQ ID NOS: 56791
 ; SOFTWARE: PatentIn ver. 2.1
 ; SEQ ID NO 38427
 ; LENGTH: 697
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa

US-10-449-902-38427
 Query Match 34.9%; Score 1078; DB 6; Length 697;
 Best Local Similarity 36.8%; Pred. No. 8.7e-72;
 Matches 262; Conservative 106; Mismatches 226; Indels 118; Gaps 13;

1 MEYRQLEZAYALIIFKSPHPNELLACKRGSQLIGNVELSGQONGKSFHDKVTLTNG 60
 185 MGENFIASQDALLPVTRPFILEGDAEITRPSVNI - FD -- -KTAGAEVKRODIESNL 239
 61 PKEULLFSSDLCIATEVTHKYNLADEDNEIWHIKDGSVSTLKFDPHKKEPKASVQRALSVLEM 120
 240 : QYDAGDKGJYRHMKQYEOPNAAIKNTLGRISHGQVDLSGPNAEELSKVEH1QIL 299
 Db 121 EVEQIKGGYDHMKQKEIHEQPHSLKTTMGRKGTVLGGJKEYL- KTIRRCRFFF 179
 QY 300 AGCTSYNSGMSVSRYWFESLAGIPCDVEIASEFPRYKSARVRNNSLMITLSQSGETADTLAG 359
 Db 180 GCGTSYNAALAAARPFEVEETGIPVMTMAYASDLDROGPIYREDTAVFVSQSGBTADTLA 239
 QY 360 LRLSKELGYLGSLAIQNFGVSSLYRESDALMTNAGBIVGASTKATTQTVLMLVAK 419
 Db 240 LDYALENLG -CVGITNTGSTLSRKTHGCVHINAGCBIQVAVTAKTQSIVAMAMMALA 298
 QY 420 LSRUQLDASIEHDVHKGQALPSPRIEONLSDQRKRIEALAEFSKDHKHALFLGRGDOIY 479
 Db 299 IGSPOIQRSTARRDIIISGANNLNSNVSEVTKLQAGMKELASSLVLGRGNYAT 358
 QY 480 ALEGALKLKEISYTHABAYAAGELKHGPALIADAMPVIVVAPPNELLKEULKNSNIEVRA 539
 Db 359 ALEGALKYKEVALMHSEGMLAGEMKHPALVDBNLPVIAITRDAFCSPKQOSVICQLLS 418
 QY 540 RGGOLYVFADQ-DAGFV - SSDNMHITEMPHAVEEVIAPFIFTYVPLQLLAYHALIKGTDV 596
 Db 419 RRGRLLIVNCRGDSASAVCPGGSCRVEVPQVADCLQVPIVNTIPLQVLLAYHTLVRGFDV 478
 QY 597 DQPNLAKSXTVE 609
 Db 479 DQPNLAKSXTVE 491

RESULT 14
 US-10-953-349-34176
 ; Sequence 34176, Application US/10953349
 ; Publication No. US20060107345A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ALEXANDROV, Nickolai et al.
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 ; TITLE OF INVENTION: ENCODED THERBY
 ; FILE REFERENCE: 2700-1579PUS2
 ; CURRENT APPLICATION NUMBER: US/10/953,349
 ; CURRENT FILING DATE: 2004-01-30
 ; NUMBER OF SEQ ID NOS: 40252
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 34176
 ; LENGTH: 488
 ; TYPE: PRT
 ; ORGANISM: Zea mays subsp. maya
 US-10-953-349-34176

Query Match 26.2%; Score 807; DB 6; Length 488;
 Best Local Similarity 37.1%; Pred. No. 6.1e-52; Indels 32; Gaps 7;

Matches 181; Conservative 96; Mismatches 179; Indels 32; Gaps 7;

QY 152 QURGAYGTVIMDSRHPDTLLAARSGLPVLIGL-----MGENF 189
 Db 3 QLEGAYALIIFKSPHPNELLACKRGSQLIGNVELSGQONGKSFHDKVTLTNGKPELF 62
 QY 190 IASDQLALLPVTRPFILEGDAEITRPSVNI - FD -- -KTAGAEVKRODIESNLQYDAG 244
 Db 63 FSSDLCIATEVTHKYNLADEDNEIWHIKDGSVSTLKFDPHKKEPKASVQRALSVLEM 122
 QY 245 DKGTYRHMKQYEOPNAAIKNTLGRISHGQVDLSGPNAEELSKVEH1QILACGTS 304
 Db 123 KRGSYDHMKQKEIHEQPHSLKTTMGRKGTVLGGJKEYL- KTIRRCRFFF 181
 QY 305 YNSGMVSRYWFESLAGIPCDVEIASEFPRYKSARVRNNSLMITLSQSGETADTLAGRLSK 364

Db 182 YNAALLAARPFEELTGIPVTMVEASDLDROGPIYREDTAVFVSQSGETADTLAIDYAL 241
 QY 365 EIGYGLS LAIQNFGVSSLYRESDALMTNAGBIVGASTKATTQTVLMLVAKUSRLK 424
 Db 242 ENGAL-CVGITNTGVTLSRTHCGWHINACCEIGVASTKATYTSQVAMAMMALAIGSDQ 300
 QY 425 GLDASLEHDIVHGLQALPSRTEQMLSDQRKRIEALAEFSKDHKHALFLGRGDOIYPLALEGA 484
 Db 301 ISTQARRDSTIISLGLNLSNNSYSEVILKLSLTDSESLVFGGRGNYATALEGA 360
 Db 121 EVEQIKGGYDHMKQKEIHEQPHSLKTTMGRKGTVLGGJKEYL- KTIRRCRFFF 179
 QY 485 LRLSKELSYTHABAYAAGELKHGPALIADAMPVIVVAPPNELLKEULKNSNIEVRA 544
 Db 361 LKVKEVAMHSEGMLGEMKHPALVDBNLPVIAITRDAFCSPKQOSVICQLLS 420
 QY 545 YYFADQ-DAGFV - SSDNMHITEMPHAVEEVIAPFIFTYVPLQLLAYHALIKGTDVQPRN 601
 Db 421 IVMCGSGDASAVCPGGSCRVEVPQVADCLQVPIVNTIPLQVLLAYHTLVRGFDVQPRN 480
 QY 602 LAKSVTVE 609
 Db 481 LAKSVTVE 488

RESULT 15
 US-10-488-015-17
 ; Sequence 17, Application US/104880015
 ; Publication No. US20060088902A1
 ; GENERAL INFORMATION:
 ; APPLICANT: STICHTING VOOR DE TECHNISCHE WETENSCHAPPEN
 ; APPLICANT: VAN DEN HONDEL, Cornelis
 ; APPLICANT: RAM, Arthur
 ; APPLICANT: DAMVELD, Robbert
 ; APPLICANT: ARENTSHORST, Mark
 ; TITLE OF INVENTION: Methods and Materials for the
 ; Identification of Antifungal Substrates in Filamentous Fungi
 ; CURRENT APPLICATION NUMBER: US/10/488,015
 ; CURRENT FILING DATE: 2004-02-27
 ; PRIORITY APPLICATION NUMBER: EP 01203423.7
 ; PRIOR FILING DATE: 2001-08-28
 ; PRIORITY APPLICATION NUMBER: PCT/EP02/09639
 ; PRIOR FILING DATE: 2002-08-28
 ; NUMBER OF SEQ ID NOS: 29
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 17
 ; LENGTH: 464
 ; TYPE: PRT
 ; ORGANISM: Aspergillus niger
 US-10-488-015-17

Query Match 19.1%; Score 589.5; DB 6; Length 464;
 Best Local Similarity 34.1%; Pred. No. 7.5e-36;
 Matches 157; Conservative 75; Mismatches 151; Indels 18 77; Gaps 9;

QY 96 VVHNGTENHEPLREELKARGTYEVSETDTEVIAHLVNVELKGQGTTLREAVL - RAIPQL 153
 Db 9 VVHNGTNTYKELKALLESKGFRFTETPCTEAKTKLYDQPDIDFTVLAKVKEI 68
 QY 154 RGAYGTVIMDSRHPDTLLAARSGLPVLIGL-----DAGDKGTVYRHMKQYEOPNAIK 265
 Db 69 EGAFGLIKSVYPHEVIAARKGSPLVIGRTSRKMKVDFDVVEYESDGPLPAEQASQNV 128
 QY 184 -----GM-----GENFIASDQLALLPVTRRFILEG 210
 Db 129 AIKSMGTLAPPDKSLLHRSQSRFLSDGGVPQPAEFFSDPAPIVETHKVLYEDD 188
 QY 211 DIAEITRPSVNF --- DKGTYAEVKRODIESNLQYDAGDKGTVYRHMKQYEOPNAIK 265
 Db 189 DIAHTHEQINTHRLTKDDTSVRAQIOTBLELQIM - KGNFDFEMKEFQDESES 246
 QY 266 NLTGRB -- ISHGQVDSLGPNAEELSKVEH1QILACGTSYNSGMVSRYWFESLAGIIPC 323
 QY 247 NTMRSRLDVAKQVTLGGJLQYI - STIRRCCRRIIFVACGTSYHSCMVAWSVFEELTEIPI 305

Qy 324 DVEIASEFYYRKSAVRNSIMIUSQSGETADTLAIGRLRISKEIYGGLSLAICNPGSSLV 383
Db 306 SVELASDFLDROAPVFRDTCVFQSGETADSLMALRVCLERGAL-TGIVNVGSSIS 364
Qy 384 RESDLALMTNAGTEIGVASTKAFTTQLTIVMLYAKLSRLKGLDASIEHDIVHGLQALPS 443
Db 365 LLTHCGVHINAGPEIGVASTKAYTSQFVAMMFAISLSDRASKQKREEIFEIMBGLAKVSE 424
Qy 444 RIEQMLSQDKRIEAL-AEFSDKHHALEFGRGDQYPIALE 482
Db 425 QFKEILKLNEPKQMCAKEFKNOKSLLLGRGGQFPTALE 464

Search completed: August 7, 2006, 09:31:32
Job time : 158 secs

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